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OM nucleic - nucleic search, using sw model

Run on: October 24, 2005, 14:55:31 ; Search time 318 Seconds
(without alignments)
8860.593 Million cell updates/sec

Title: US-09-721-183-18

Perfect score: 1722

Sequence: 1 tgcaccagatgactctgaa.....acaaaaaaaaaaaaaa 1722

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1592.2	92.5	1708	4	US-09-949-016-2595 Sequence 2595, Ap
2	1536.8	89.2	1629	4	US-09-949-016-2596 Sequence 2596, Ap
3	1478	85.8	1854	4	US-09-356-806-39 Sequence 39, Appl
4	1395.4	81.0	1832	4	US-09-949-016-2734 Sequence 2734, Ap
5	1375.6	79.9	2092	4	US-09-356-806-7 Sequence 7, Appli
6	1370.8	79.6	2092	4	US-09-949-016-2594 Sequence 2594, Ap
7	1370.8	79.6	2092	4	US-09-949-016-3181 Sequence 3181, Ap
8	1364.4	79.2	2093	4	US-09-949-016-1128 Sequence 1128, Ap
9	1219.2	70.8	2107	3	US-09-180-852-1 Sequence 1, Appli
10	1213.6	70.5	1976	4	US-09-356-806-112 Sequence 112, App
11	1151.8	66.9	1413	3	US-09-813-918-1 Sequence 1, Appli
12	1151.8	66.9	1413	4	US-10-060-311-1 Sequence 1, Appli
13	962.2	55.9	1323	4	US-09-949-016-2735 Sequence 2735, Ap
14	962.2	55.9	1323	4	US-09-949-016-2736 Sequence 2736, Ap
15	754.8	43.8	2966	4	US-09-976-594-241 Sequence 241, App
16	680.2	39.5	18373	4	US-09-949-016-14338 Sequence 14338, A
17	680.2	39.5	18452	4	US-09-949-016-14337 Sequence 14337, A
18	638.2	37.1	1001	4	US-09-671-317-403 Sequence 403, App
19	608.2	35.3	1686	4	US-09-356-806-41 Sequence 41, Appl
20	584.8	34.0	1323	4	US-09-356-806-1 Sequence 1, Appli
21	584.8	34.0	19732	4	US-09-949-016-12870 Sequence 12870, A
22	584.8	34.0	19732	4	US-09-949-016-14923 Sequence 14923, A
23	584.8	34.0	19733	4	US-09-949-016-14336 Sequence 14336, A
24	525.6	30.5	20441	4	US-09-949-016-14476 Sequence 14476, A
25	498.8	29.0	2312	4	US-09-356-806-114 Sequence 114, App
26	497.2	28.9	20599	4	US-09-949-016-14477 Sequence 14477, A
27	497.2	28.9	20599	4	US-09-949-016-14478 Sequence 14478, A

ALIGNMENTS

RESULT 1

US-09-949-016-2595
; Sequence 2595, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2595

; LENGTH: 1708

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-2595

Query Match 92.5%; Score 1592.2; DB 4; Length 1708;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 1645; Conservative 0; Mismatches 63; Indels 5; Gaps 1;

QY	1	TGACACAGGATGACTCTGAATCGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTAC	60
DB	1	TGACACAGGATGCTTCTGAATGGCTTCAGTTCTTCTGCTGATACATCTCAGTTGTAC	60
QY	61	TTTAGCTCTGGGAGTTGTGAAAAGTCTGGTGTGGCCGACAGAAATACAGCCATTGGATG	120
DB	61	TTTAGCTCTGGGAGTTGTGAAAAGTCTGGTGTGGCCGACAGAAATACAGCCATTGGATG	120
QY	121	AATATGAAGCAATCTCTGAAGAGCTGTTTCAGAGAGGTATGAGAGTACTGTTACTGGCA	180
DB	121	AATATGAAGCAATCTCTGAAGAGCTGTTTCAGAGAGGTATGAGAGTACTGTTACTGGCA	180
QY	181	TCTTCAGCTTCCATTCTTTTGTATCCCAATGATGCATCCACTCTTAATTTGAAGTTAT	240
DB	181	TCTTCAGCTTCCATTCTTTTGTATCCCAATGATGCATCCACTCTTAATTTGAAGTTAT	240
QY	241	CCTACATCTTTAACTAAACTGAATTTGAGAATATCATGCAACAGGTTAAGAGATGG	300
DB	241	CCTACATCTTTAACTAAACTGAATTTGAGAATATCATGCAACAGGTTAAGAGATGG	300
QY	301	TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTTCAAGAACAGAAATCCTGTGG	360

Sequence 412, Appl
Sequence 45, Appl
Sequence 405, Appl
Sequence 2, Appli
Sequence 76, Appli
Sequence 1813, Ap
Sequence 6, Appli
Sequence 352, App
Sequence 353, App
Sequence 354, App
Sequence 17, Appl
Sequence 118, App
Sequence 427, App
Sequence 3284, Ap
Sequence 424, App
Sequence 428, App
Sequence 404, App

Db 302 TCAGACATTCCTCAAGAGATACATTTGGTTATATTTTCAAGAAACCAAGAAATCGCTGTAG 361
Qy 361 GAATATATACATATTTAGAAATCTCTGTAAGATGTAGTTTCAATATAGAAAGTTATG 420
Db 362 GAATATATACATATTTAGAAATCTCTGTAAGATCTCAATTTCAATAAGAAATTTATG 421
Qy 421 AAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTCCCTCTGGT 480
Db 422 AAAAACTATAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTTTTTTCCCTGTGGT 481
Qy 481 GAGTCTGCTGCTGCTGCTTAAACATACAGTTTGTGTACAGTCTCCGCTTTACTCTGGC 540
Db 482 GAGTCTGCTGCTGCTGCTTAAACATACAGTTTGTGTACAGTCTCCGCTTTACTCTGGC 541
Qy 541 TACACAAATGAAAGGACAGTGGAGGACTGATTTTCCCTCTTACATACATCTATTGTT 600
Db 542 TACACAGTTGAAAGGACAGTGGAGGACTGATTTTCCCTCTTACATACATCTATTGTT 601
Qy 601 ATGTCAAAATTAAGTGTATCAAAATGACATTTTCATGGAGAGGTTAAAAATATGATCTATGTG 660
Db 602 ATGTCAAAATTAAGTGTATCAAAATGACATTTTCATGGAGAGGTTAAAAATATGATCTATGTG 661
Qy 661 CTTTATTTTGAATTTGGTTCCAAATGCTCTGATATGAAGAGTGGGATCAGTTTTTACAGT 720
Db 662 ATTTATTTTGAATTTGGTTCCAAATATGTATATGAAGAGTGGGATCAGTTTTTACAGT 721
Qy 721 GAAGTTTATAGGAGACCACTACCTTATTTGAGACATGGAAGCTGACATATGGCTT 780
Db 722 GAAGTTTATAGGAGACCACTACCTTATTTGAGACATGGAAGCTGACATATGGCTT 781
Qy 781 ATGCAAACTCTGAGTGTTCATTTTCCCTCATCTTCTTACCAACGTTGATTTTGT 840
Db 782 ATGCAAACTCTGAGTGTTCATTTTCCCTCATCTTCTTACCAACGTTGATTTTGT 841
Qy 841 GGAGGATTCATCTGCAAACTGCAAAACCCCTACCTAAGGAATGGAGGAGTTGTACAG 900
Db 842 GGAGGATTCATCTGCAAACTGCAAAACCCCTACCTAAGGAATGGAGGAGTTGTACAG 901
Qy 901 AGCTCTCGAGAAATGTTGTGTTGTTCTCTGGGTCAGTGAAAGTAAACATGACA 960
Db 902 AGCTCTCGAGAAATGTTGTGTTGTTCTCTGGGTCAGTGAAAGTAAACATGACA 961
Qy 961 GCAGAAAGGCGCAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAAGTTCTGTG 1020
Db 962 GCAGAAAGGCGCAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAAGTTCTGTG 1021
Qy 1021 AGATTTGACGGGAATAAACAGATGCTTCTAGGTCCTCAATCTCGGCTGTACAGTGATA 1080
Db 1022 AGATTTGATGGGAATAAACAGATGCTTCTAGGTCCTCAATCTCGGCTGTACAGTGATA 1081
Qy 1081 CCCCAGAAATGACCTTCTAGGTCATCCAAACACAGAGCTTTTATACTCATGTTGGAGCC 1140
Db 1082 CCCCAGAAATGACCTTCTAGGTCATCCAAACACAGAGCTTTTATACTCATGTTGGAGCA 1141
Qy 1141 AATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGTTGGGCAATCCATTTGTTGG 1200
Db 1142 AGTGGCATCTATGAGGCAATCTACCATGGGATCCCTATGTTGGGCAATCCATTTGTTGG 1201
Qy 1201 GATCAACCTGATATGCTTCAATGAGGCGCAAGGGAGCAGCTGTTAGATTGGACTTC 1260
Db 1202 GATCAACCTGATATGCTTCAATGAGGCGCAAGGGAGCAGCTGTTAGATTGGACTTC 1261
Qy 1261 AACCAATGTGAGTACAGACCTCTGAATGCTGAGGAGTAAATTAATGATCCCTTTA 1320
Db 1262 CACCAATGTGAGTACAGACCTCTGAATGCTGAGGAGTAAATTAATGATCCCTTTA 1321
Qy 1321 TATAAGAGAAATATTAAGAAATTAACAGAAATCAACATGATCAACAGTAAAGCCCTG 1380
Db 1322 TATAAGAGAAATATTAAGAAATTAACAGAAATCAACATGATCAACAGTAAAGCCCTG 1381
Qy 1381 GATCGAGAGTCTTCTGGAATTTGTCATGCCCCCAAGAGGCGCAACACCTTCGA 1440

Db 1382 GATCGAGAGTCTTCTGGAATTTGTCATCGGCCACAAAGAGGCCAAACACCTTCGA 1441
Qy 1441 GTTGCAGCCCATGACCTCAGCTGTTCCAGTACCACCTCTTTGGATGTGATTTGGGTTTCTG 1500
Db 1442 GTTGCAGCCCGTACCTCAGCTGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTCG 1501
Qy 1501 CTGGCTGTGTGGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTTTGTCTGG 1560
Db 1502 CTGGCTGTGTGGCAACTGTGATATTTATCATCAAAAGTGTGTCTGTTTGTCTGG 1561
Qy 1561 AAGTTTCTAGAAAGGAGAGGAGGAAAGAGATTTAGTTATGTCTGACATTTGAAGCT 1620
Db 1562 AAGTTTCTAGAAAGTGTGAAAGAGGAAAGGATTTAGTTATGTCTCGACATTTGAAGCT 1621
Qy 1621 GGAAGAAC 1628
Db 1622 GGAAGAAC 1629

RESULT 3

US-09-356-806-39
; Sequence 39, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and
; FILE OF INVENTION: 2B15 (UGT2B15) Genes
; FILE REFERENCE: SEQ-22PRV2
; CURRENT APPLICATION NUMBER: US/09/356, 806
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15) ... (1584)
US-09-356-806-39

Query Match 85.8%; Score 1478; DB 4; Length 1854;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1577; Conservative 0; Mismatches 140; Indels 5; Gaps 1;

Qy 1 TGCACCAAGGATGCTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTAC 60
Db 6 TGCACCAAGGATGCTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTAC 65
Qy 61 TTTAGTCTCGGAGTTGTGAAAAGTCTGTTGGGCGCCAGAGATCAGCCATTTGATG 120
Db 66 TTTAGTCTCGGAGTTGTGAAAAGTCTGTTGGGCGAGAGATACAGCCATTTGATG 125
Qy 121 AATATGAAGCAATCTCCGAAAGAGCTTTTCAGAGAGGTCTAGAGTCTGACTGCTGCA 180
Db 126 AATATAAGACAATCTCGGATGAGCTTTTCAGAGAGGTCTAGAGTCTGACTGCTGCA 185
Qy 181 TCTTCAAGTCTCCATTTCTTTTGTATCCCAATGATGCTCCTTAAATTTGAAGTTTAT 240
Db 186 TCTTCAAGTCTCCATTTCTTTTGTATCCCAACACTCATCCGCTCTTAAATTTGAATTTAT 245
Qy 241 CCTACATCTTTAACTAAACCTGAAATTTGAGATATCATCATGCAAGGTTTAAGAGATGG 300
Db 246 CCCACATCTTTAACTAAACCTGAGTTGGAGAAATTCATCATGCAACAGATTAAGAGATGG 305
Qy 301 TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAAGAACAAAGAAATCCTGTGG 360
Db 306 TCAGACCTTCCAAAAGATACATTTGGTTATATTTTTCACAAAGTACAGGAATCATGTCA 365

QY 361 GAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAATAAGAAAGTTATG 420
Db 366 ATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAATAAGAAATTTATG 425
QY 421 AAAAACTACAAGATCAAGATTGTGACATCGTTTTTGGCAGATGCTGTTTTTCCCTGTGGT 480
Db 426 AAAAAAGTACAAGATCAAGATTGTGACATCGTTTTTGGCAGATGCTATTTTTTCCCTGTAGT 485
QY 481 GAGCTGCTGGCTCGCTTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTTACTCTCTGGC 540
Db 486 GAGCTGCTGGCTGAGCTATTTAAACATACCCTTTGTGTACAGTCTCAGCTTCTCTCTGGC 545
QY 541 TACAACATTTGAAGGCACAGTGGAGGACTGAATTTCCCTCTTCCACATACCTATTGTT 600
Db 546 TACACTTTTGAAGGCATAGTGGAGGATTTATTTTCCCTCTTCCACATACCTATTGTT 605
QY 601 ATGTCAAAATTAAGTCAATCAATGACTTTCATGGAGGGTAAATAATATGATCTATGTG 660
Db 606 ATGTCAAAATTAAGTCAATCAATGACTTTCATGGAGGGTAAATAATATGATCTATGTG 665
QY 661 CTTTATTTTGGCTTTGGTTCCAAATGCTCTGATATGAAGAGTGGATCAGTTTTTACAGT 720
Db 666 CTTTATTTTGGCTTTGGTTCCAAATGCTCTGATATGAAGAGTGGATCAGTTTTTATAGT 725
QY 721 GAAGTTTATAGGAAGACCCACTACTTATTTTGACAAATGGGAAAGCTGACATATAGCTT 780
Db 726 GAAGTTTCTAGGAAGACCCACTACTATTTCTGAGACAAATGGGAAAGCTGACGTTAGCTT 785
QY 781 ATCGAAACTCTGGAGTTTCAATTTCTCTCATCCATTTCTTACCAACGTTGATTTGTT 840
Db 786 ATTCGAAACTCTCTGGAAATTTTCAGTTTCTCATATCCACTCTTACCAAAATGCTATTTGTT 845
QY 841 GGAGGATTCACATGCAAACTGCAAACTCCCTACCTAAGCAATGAGGAGTTTGTACAG 900
Db 846 GGAGGACTCACATGCAAACTGCAAACTCCCTGCTTAAAGCAATGGAAGACTTTGTACAG 905
QY 901 AGCTCTGGAGAAATAGTGTGTGTGTGTTTCTCTGGGGTCACTGATATAACATGACA 960
Db 906 AGCTCTGGAGAAATAGTGTGTGTGTGTTTCTCTGGGGTCAATGCTCAGTAACATGACA 965
QY 961 GCAGAAAGGCCAATGTAATTTGCAAAAGCCCTTGGCCAAAGATCCCAAAAGGTTCTGTGG 1020
Db 966 GAAGAAAGGCCAACGTAATTTGCAATGAGCCCTGGCCAGATCCCAAAAGGTTCTGTGG 1025
QY 1021 AGATTTTACGGGAATAAACCAGATGCTTAGGTCTCAATACCTCGGCTGTACAGTGGATA 1080
Db 1026 AGATTTTACGGGAATAAACCAGATGCTTAGGTCTCAATACCTCGGCTGTACAGTGGATA 1085
QY 1081 CCCAGAAATGACCTTCTAGGTATCCAAAAACCAGAGCTTTTATAACTCATGGTGAGCC 1140
Db 1086 CCCAGAAATGACCTTCTAGGTATCCAAAGACAGAGCTTTTATAACTCATGGTGAGCC 1145
QY 1141 AATGGCATCTATAGGCAATCTACCAATGGGATCCCTATGGTGGGCAATTCATTTGTTTTT 1200
Db 1146 AATGGCATCTACAGGCAATCTACCAATGGGATCCCTATGGTGGGATTCATTTGTTGCG 1205
QY 1201 GATCACTCTGATAAATGCTCATATGAAGGCAAGGAGGAGCTGTTAGATTGGAATTC 1260
Db 1206 GATCACTCTGATAAATGCTCATATGAAGGCAAGGAGGAGCTGTTAGATTGGAATTC 1265
QY 1261 AACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTTTA 1320
Db 1266 AACACAATGTCGAGTACAGCTTGTGAATGCACTGAAGAGAGTAATTAATGATCCTTCA 1325
QY 1321 TATAAGAGAAATATTATGAATTTATCAAGAAATCAACATGATCAACAGGTAAGCCCTTG 1380
Db 1326 TATAAGAGAAATATTATGAATTTATCAAGAAATCAACATGATCAACAGGTAAGCCCTTG 1385
QY 1381 GATCGAGAGCTCTCTGGATTGAATTTGTCATGCCCAAGGAGGCCAAACACCTTCGA 1440
Db 1386 GATCGAGAGCTCTCTGGATTGAATTTGTCATGCCCAAGGAGGCCAAACACCTTCGG 1445
QY 1441 GTTGCAGCCCATGACCTCACCTGGTTTCCAGTACCACCTCTTTGGATGTGATGGTTTCTG 1500

Db 1446 GTTGCAGCCACGACCTCACCTGGTTCCAGTACCACCTCTTTGGATGTGATGGTCTCTG 1505
QY 1501 CTGGCTCTGTGGCAACTCTGTATATTTATCATCAAAAGTTTTGTCTGTCTTTCTCTGG 1560
Db 1506 CTGGCTCTGTGGCAACTCTGTATATTTATCGTCACAAAATGTTGTCTGTCTTTCTCTGG 1565
QY 1561 AAGTTTGTAGAAAAGGGGAAGGAAAGAGATTAGTTATGTCTGACATTTGAAGCT 1620
Db 1566 AAGTTTGTAGAAAAGGCAAGGAAAGGAAATATGATTATCTGAGATTGAAGCT 1625
QY 1621 GGAAAAACCATAGATAGGACAACTTCAGTTTATTTCCAGCAAGAAAAGATTGTTAT 1680
Db 1626 GGAAAAACCTGATAGGTGAGACTTACTTCAGTTTATTTCCAGCAAG-----AAAGATTGTTAT 1680
QY 1681 GCAAGATTCTTTCTTCTCTCTGTCACAAAAAAGAAAAA 1722
Db 1681 GCAAGATTCTTTCTTCTCTGAGACAAAAAAGAAAAA 1722

RESULT 4
US-09-949-016-2734
; Sequence 2734, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2734
; LENGTH: 1832
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1832)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-2734

Query Match 81.0%; Score 1395.4; DB 4; Length 1832;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 156; Indels 30; Gaps 3;
QY 1 TGCACCAGGATGACCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTTAC 60
Db 6 TGCACCAGGATGCTGTGAAATGGACTTCAGTAATTTTCTTAATACAACTGAGCTTTTC 65
QY 61 TTTAGCTCTGGAGTTGTGGAAAAAGTGTGGTGTGGCCGCGAGAAATACAGCCATTGGATG 120
Db 66 TTTAGCTCTGGAAATTTGGAAAGGTGTGGTGTGGCGAGCAGAAATACAGCCATTGGATG 125
QY 121 AATATTGAGACAACTCCTGAAAGAGCTTGTTCAGAGAGGTGTCAGGTGACTGTACTGGCA 180
Db 126 AATATAAGACAACTCCTGGATGAGCTTATTCAGAGGTCATGAGGTGACTGTACTGGCA 185
QY 181 TCTTCAGCTTCCATTTCTTTTGTATCCCAATGATGATCCACTCTTTAAATTTGAAGTTTAT 240
Db 186 TCTTCAGCTTCCATTTCTTTTGTATCCCAACTCATCGCTCTTTAAATTTGAAATTTAT 245
QY 241 CCTACATCTTTAACTTAAACTGAAATTTGAGAATATCATCATCAACAGGTTAAGATGG 300
Db 246 CCCACATCTTTA-----ANNNNNNNNNNNNNNNTTGG 281

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Qy 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTTCAAGAACA-AGAAATCCTGTG 359
Db 282 TCAGACCTTCGAAAGATACATTTTGGTTATATTTTTTCAAGGTACAGGGAATCATGTC 341
Qy 360 GGAATTATGACATATTTAGAACTTCTGTAAAGATGTAGTTTCAAAATGAAGAAATTAT 419
Db 342 AATATTTGGTGACATAAATAGAAAGTTCTGTAAAGATGTAGTTTCAAAATGAAGAAATTAT 401
Qy 420 GAAAAAATCAAGAGTCAAGATTGACATCGTTTTCAGAGTCTGTTTTCCTCTGG 479
Db 402 GAAAAAGTACAGAGTCAAGATTGACGTATTTTTCAGAGTCTATTTTTCCTCTAG 461
Qy 480 TGAGCTCTGCTGCTGCTACTTAACATACACGTTTGTGTACAGTCTCCGCTTTTACTCTCG 539
Db 462 TGAGCTCTGCTGCTGCTACTTAACATACACCTTTGTGTACAGTCTCAGCTTCTCTCCTG 521
Qy 540 CTACACAAATGAAAGGCACAGTGGAGGACTGATTTTCCCTCTCTACATACCTATTGT 599
Db 522 CTACACATTTTGAAGAGCATAGTGAGGATTTATTTTCCCTCTCTACGTAACCTGTTGT 581
Qy 600 TATGTCAAAATTAAGTGCATCAATGACTTTTCAATGAGAGGTTAAATAATATGATCTATGT 659
Db 582 TATGTCAGAATTAAGTGCATCAATGACTTTTCAATGAGAGGTTAAATAATATGATCTATGT 641
Qy 660 GCTTTATTTGACTTTTGGTTTCCAAATGTCTGATATGAAGAGTGGATCAGTTTTCAG 719
Db 642 GCTTTACTTTGACTTTTGGTTTTCGAAATATTTGACATGAAGAGTGGATCAGTTTTCAG 701
Qy 720 TGAAGTTTGAAGAGCCACTACTTATTTGAGACAAATGGGAAAGCTGACATATGGCT 779
Db 702 TGAAGTTTGAAGAGCCACTACTTATTTGAGACAAATGGGAAAGCTGACATATGGCT 761
Qy 780 TATCGGAACTCTGAGTTTTCATTTTCTCATCCATTTCTACCAACGTTGATTTTGT 839
Db 762 TATTCGAACTCTGAGTTTTCATTTTCTCATCCATTTCTACCAACGTTGATTTTGT 821
Qy 840 TGGAGGATTCACCTGCAAACTGCCAAACCCCTACCTAAGAAATGAGGAGTTTGTACA 899
Db 822 TGGAGGACTCCACTGCAAACTGCCAAACCCCTACCTAAGAAATGAGGAGTTTGTACA 881
Qy 900 GAGCTCTGGAGAAATGGTGTGGTGTGTTTCTCTGGGTGCTAGTGAATAGTAACATGAC 959
Db 882 GAGCTCTGGAGAAATGGTGTGGTGTGTTTCTCTGGGTGCTAGTGAATAGTAACATGAC 941
Qy 960 AGCAGAAAGGCGCAATGTAAATTGCAACAGCCCTTGCCAAAGTCCCAAAAGGTTCTGTG 1019
Db 942 AGAAGAAAGGCGCAACGTAAATTGCAATGAGTCAAGCCCTGCCAGATCCCAAAAGGTTCTGTG 1001
Qy 1020 GAGATTTGACGGGAATAAACCCAGATGCTTAGGTCTCAATCTCGGCTGTACAGTGGAT 1079
Db 1002 GAGATTTGATGGGAATAAACCCAGATACCTTAGGTCTCAATCTCGGCTGTATAGTGGAT 1061
Qy 1080 ACCCAGAAATGACCTTCTAGTCTATCCAAAACCCAGAGCTTTTATACTCATGTGGAGC 1139
Db 1062 ACCCAGAAATGACCTTCTAGTCTATCCAAAACCCAGAGCTTTTATACTCATGTGGAGC 1121
Qy 1140 CAATGGCATCTATGAGGCAATCTACCATGGATCCCTATGTTGGGCATTCATTTGTTTTT 1199
Db 1122 CAATGGCATCTACGAGGCAATCTACCATGGATCCCTATGTTGGGCATTCATTTGTTTC 1181
Qy 1200 TGATCAACCTGATTAACATTTGCTACATGAAGGCCAAGGGAGCAGCTGTAGATTTGACTT 1259
Db 1182 CGATCAACCTGATTAACATTTGCTACATGAAGGCCAAGGGAGCAGCTGTAGATTTGACTT 1241
Qy 1260 CAACACAAATGTCGAGTACAGACCTGCTGAATGCACTGAAGCAGTAATTAATGATCTTTT 1319
Db 1242 CAACACAAATGTCGAGTACAGACCTGCTGAATGCACTGAAGCAGTAATTAATGATCTTTT 1301
Qy 1320 ATATAAGAGAAATTTATGAATTTATCAAGAAATTAACATGATCAACAGTAAGAGCCCT 1379
Db 1302 ATATAAGAGAAATTTATGAATTTATCAAGAAATTAACATGATCAACAGTAAGAGCCCT 1361
Qy 1380 GGATCGAGCAGTCTTCTGGATTGAATTTGTCTATGCCCCCAAGAGGAGCCAAACACCTTCG 1439
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Db 1362 GGATCGAGCAGTCTTCTGGATTCAATTTTGTCTATGCGCCACAAAGGAGCTAAACACCTTCG 1421
Qy 1440 AGTTGAGCCCATGACCTCACCTGGTTCAGTACCACCTCTTTGGATGTGATTGGGTTCT 1499
Db 1422 GGTGAGCCCATGACCTCACCTGGTTCAGTACCACCTCTTTGGATGTGATTGGGTTCT 1481
Qy 1500 GCTGGGCTGTGTGGCACTGTGATATTTATCATCAAAAGTTTGTCTGTTTCTGTTCTG 1559
Db 1482 GCTGGTCTGTGTGGCACTGTGATATTTATCGTCACAAATATTTGCTGTTTCTGTTCTG 1541
Qy 1560 GAAGTTTGTAGAAAAAGGGAAGGGAAGGGAAGGGAAGGATTTAGTTATGCTGACATTTGAAGC 1619
Db 1542 GAAGTTTGTAGAAAAAGGGAAGGGAAGGGAAGGGAAGGATTTAGTTATGCTGACATTTGAAGC 1601
Qy 1620 TGGAAACACAGATAGATAGGACAACTTTCAGTTTATTTCCAGCAAGAAAGAAAGATTGTTA 1679
Db 1602 TGGAAACCTGATAGGTGAGACTACTTCAGTTTATTTCCAGCAAG-----AAAGATTGTGA 1656
Qy 1680 TGAAGATTTCTTTCTTCTCTGTGACAAAAAAGGGAAGGGAAGGGAAGGGAAGGGAAGG 1722
Db 1657 TGAAGATTTCTTTCTTCTCTGTGACAAAAAAGGGAAGGGAAGGGAAGGGAAGGGAAGG 1699

RESULT 5
US-09-356-806-7
; Sequence 7, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UCT2B4), 2B7 (UCT2B7) and
; FILE REFERENCE: SEQ-22PRV2
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2092
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (38)...(1621)
; US-09-356-806-7

Query Match 79.9%; Score 1375.6; DB 4; Length 2092;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1525; Conservative 0; Mismatches 189; Indels 6; Gaps 3;

Qy 1 TGACACGAGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTTCAC 60
Db 29 TGCATCAGGATGCTATGAAATGGACTTCAGTCTTCTGCTGATACAGCTGAGCTGTTCAC 88
Qy 61 TTTAGCTCTGGGAGTTCTGGAAGAGTCTGTTGGGCCGCGCAGAAATACAGCCATTGGATG 120
Db 89 TTTAGCTCTGGGAGTTCTGGAAGAGTCTGTTGGGCCGCGCAGAAATTCAGCCACTGGATG 148
Qy 121 AATATGAAGACAATCTCTGAAAGAGCTTGTTCAGAGAGGTGATGAGGTGACTGTACTGGCA 180
Db 149 AATATAAGACAATCTCTGGATGAATTTGCCAGAGAGGTGATGAGGTGACTGTATTGGCA 208
Qy 181 TCTTACGCTTCCATCTCTTTTGTATCCCAATGATGTCATCCACTCTTAATTTGAAGATTAT 240
Db 209 TCTTACGCTTCCATCTCTTTTGTATCCCAATGATGTCATCCACTCTTAATTTGAAGATTAT 268
Qy 241 CCTACATCTTTAACTAAACATGAATTTGAGAATATCATCATCAACAGGTTTAAGAGATGG 300
Db 269 CCTGTATCTTTAACTAAACATGAATTTGAGGATATTTATCAAGCAGCTGGTTTAAGAGATGG 328
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QY 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATATTTTTCACAGAACACAGAAATCCCTGTGG 360
Db 329 GCAGAACTTCCAAAAGACACATTTTGGTCATATTTTTCACAAAGTACAAAGAAATCATGTGG 388
QY 361 GAATTAATGACATATTTAGAACTTCTGTAAGATGTAGTTTCAAAATAGAAGATTATG 420
Db 389 ACATTTAATGACATATTTAGAAAGTTCTGTAGGATATAGTTTCAAAATAGAAGATTATG 448
QY 421 AAAAACTACAAGATCAAGATTTGACATCGTTTTTTGCGAGATCGTTTTTCCCTGTGGT 480
Db 449 AAGAAACTACAGGAGTCAAGATTGTATGTGTTCTTTGCGAGATCGTTTTTCCCTTTGGT 508
QY 481 GAGCTGCTGGCTGGCTACTTAACATACGGTTTTGTGTACAGTCTCCGCTTTACTCTCGGC 540
Db 509 GAGCTGCTGGCCGAGTTACTTAAAAATACCCTTTTGTCTACAGCCTCCGCTTCTCTCGGC 568
QY 541 TACACAATTTGAAAGGCACAGTGGAGACTGATTTTCCCTCTTCCCTACATACCTATTGTT 600
Db 569 TACCGAATTTGAAAGCATAGTGGAGACTTCTGTTCCCTCTTCCCTATATGCGCTGTGTT 628
QY 601 ATGTCAAAATTAAGTGAATCAATGACATTTATGAGAGAGGTTAAAAATATGATCTATGTG 660
Db 629 ATGTCAGAACTAAGTGACCAAAATGACTTTTCATAGAGAGGTTAAAAATATGATCTATGTG 688
QY 661 CTTTATTTTGGCTTTGGTTCCAAATGCTCTGATATGAAGAGTGGGATCAGTTTTCACGT 720
Db 689 CTTTATTTTGAATTTTGGTTTCCAAATATTTTGACATGAAGAGTGGGATCAGTTTTCACGT 748
QY 721 GAAGTTTTAGGAAGACCCACTAGCTTATTTTGACACAAATGGGAAAGCTGACATATGGCTT 780
Db 749 GAAGTTCTAGGAAGACCCACTAGCTTATCTGAGACAAATGGCAAAAGCTGACATATGGCTT 808
QY 781 ATGCGAACTCTGGAGTTTTTCAATTTCCCTCATCCATTCTTACCAAACGTTGATTTGTT 840
Db 809 ATTCGAAACTACTGGGATTTTCAATTTCCCTCACCCACTCTTACCAAATGTGAGTTGCTT 868
QY 841 GGAGGATTCACATGCAAACTGCAAAACCCCTACCTAAGGAATGAGGAGTTGTGTACAG 900
Db 869 GGAGGACTCACATGCAAACTGCAAAACCCCTACCGAAGCAATGGAAGAGTTGTGCCAG 928
QY 901 AGCTCTGGAGAAATGGTGTGTGTGTTTCTCTGGGGTCAAGTATAGTAAATACATGACA 960
Db 929 AGCTCTGGAGAAATGGTGTGTGTGTTTCTCTGGGGTCAAGTATAGTAAATACATGACA 988
QY 961 GCAGAAAGGCCAATGTAAATTTGCAACAGCCCTTGGCCAAAGATCCCAAAAAGTTCTGTGG 1020
Db 989 GAAGAAAGGCCAATGTAAATTTGCATCAGCCCTTGGCCAAAGATCCCAAAAAGTTCTGTGG 1048
QY 1021 AGATTTGACGGGAATAAACAGATGCTTAGGTCTCAATACTCGGCTGTACAGTGGATA 1080
Db 1049 AGATTTGATGGGAATAAACAGATGCTTAGGTCTCAATACTCGGCTGTACAGTGGATA 1108
QY 1081 CCCAGAATGACCTTCTAGGTCTATCCAAAACACAGAGCTTTTATACTCATGTGTGGAGCC 1140
Db 1109 CCCAGAGATGATCTTCTGGTCAACCAAAACACAGAGCTTTTATACTCATGTGTGGAGCC 1168
QY 1141 AATGGCATCTATAGGGAATCTACCAATGGGATCCCTTATGTTGGGCATTTCCATTTGTTTTT 1200
Db 1169 AATGGCATCTATAGGGAATCTACCAATGGGATCCCTTATGTTGGGCATTTCCATTTGTTTGA 1228
QY 1201 GATCAACCTGATAAATGCTCATGTAAGGCCAAGGCGAGCTGTTAGATTTGGACTTC 1260
Db 1229 GATCAACCTGATAAATGCTCATGTAAGGCCAAGGCGAGCTGTTAGATTTGGACTTC 1288
QY 1261 AACCAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCCTTTA 1320
Db 1289 CACACAATGTCGAGTACAGACTTACTCAATGCACTCAAGACAGTAATTAATGATCCCTTTA 1348
QY 1321 TATAAGAGATATTTATGAAATTTATCAAGAAATTTCAACATGATCAACAGGTAAAGCCCTG 1380
Db 1349 TATAAGAGATGCTATGAAATTTATCAAGAAATTTATCAAGAAATTTATCAAGAGTAAAGCCCTT 1408
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QY 1381 GATCAGCAGTCTTCTGGATTGAATTTGTCTATGCCCAAGAGGCCAAACACCTTCGA 1440
Db 1409 GATCAGCAGTCTTCTGGATTGAATTTGTCTATGCCCAAGAGGCCAAAGCACCTTCGG 1468
QY 1441 GTTGAGCCCATGACCTCACCTGGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTCTG 1500
Db 1469 GTTGAGCCCATGACCTCACCTGGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTCTG 1528
QY 1501 CTGGCTGTGTGGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTGTTTGTCTG 1560
Db 1529 CTGGCTGTGTGGCAACTGTGATATTTATCATCACAAAA---ATGCTGTGTTGTGCTGG 1585
QY 1561 AAGTTTGTAGAAAAGGGAAGGAAAGAGATTAGTATGCTGTGACATTTGAAGCT 1620
Db 1586 AAGTTTGTAGAACAGGAAAGGGAAGAGATTAAATTACGTCTGAGGCTGGAAGCT 1645
QY 1621 GGAAACACAGATAGATAGGACAACTTCAGTTTATTTCCAGCAAGAAAGAAAGATTCTTAT 1680
Db 1646 GGGAAACCAATAAAT-GAATCCCTTTAGTTTATTACAACAAGAA--GACGTTGTGATAC 1702
QY 1681 GCAAGATTTCTTCTCTCTGTGACAAAAAATAAAAAA 1720
Db 1703 AAGAGATTCCTTCTTCTTGTGACAAAAACATCTTTCAAAA 1742

RESULT 6
US-09-949-016-2594
; Sequence 2594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2594
; LENGTH: 2092
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2594

Query Match 79.6%; Score 1370.8; DB 4; Length 2092;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 192; Indels 6; Gaps 3;

QY 1 TGCACAGAGTACCTGAAATGGACTTTCAGTTCTTCTGCTGATACATCTCAGTTCTTAC 60
Db 29 TGCATCAGAGTCTATGAATGGACTTCAGCTCTTCTGCTGATACAGCTGAGCTGTAC 88
QY 61 TTTAGCTCTGGAGTTGTGAAAAGTGTGTTGGGCCGAGAAATACAGCAATTTGGATG 120
Db 89 TTTAGCTCTGGAGTTGTGAAAAGTGTGTTGGGCCGAGAAATTCAGCCACTGGATG 148
QY 121 AATATGAAAGCAATCTCTGAAGAGCTTGTTCAGAGAGTTCATGAGTGTACTGTAC 180
Db 149 AATATAAAGACAAATCTCTGGATGAATTTGTCAGAGAGGTCATGAGGTGACTGTAT 208
QY 181 TCTTCAGCTTCCATTTCTTTTGTATCCCAATGATGATCCACTCTTAAATTTGAAGTTTAT 240
Db 209 TCTTCAGCTTCCATTTCTTTTGTATCCCAACAGCCCATCTACTCTTAAATTTGAAGTTTAT 268
QY 241 CCTCATCTTTAACTAAACTGAAATTTTGAGAAATATCATCATGCAACAGGTTTAAGAGATGG 300
Db 269 CCTGTATCTTTAACTAAACTGAGTTTGAGGATATTTATCAAGCAGCTGTTTAAGAGATGG 328
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Qy 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAAAGAACAGAAATCCTGTGG 360
Db |||||
Qy 329 GCAGAACTTCCAAAAGACACATTTTGGTCATATTTTTCACAAAGTACAAAGAAATCATGTGG 388
Db |||||
Qy 361 GAATTTATGACATATTTAGAACTTCTGTHAAGATGATGTTTCAATATAGAAAGTTATG 420
Db |||||
Qy 389 ACATTTTAATGACATATTTAGAAAGTCTGTGAAGATATAGTTTCAAAATAGAAACTTATG 448
Db |||||
Qy 421 AAAAACTTACAAGAGTCAAGATTTTACATCGTTTTCAGAGATGCTGTTTTCCTCTGGT 480
Db |||||
Qy 449 AAAAACTTACAGGAGTCAAGATTTTATGTTGTTCTTGAGAGTCTGTTTCCCTTTGGT 508
Db |||||
Qy 481 GAGCTGCTGGCTACTTAAACATAGGTTTGTGACAGTCTCCGCTTTACTCTCTGGC 540
Db |||||
Qy 509 GAGCTGCTGGCGAGTTACTTTAAATACCTTTGCTACAGCTCCGCTCTCTCTGGC 568
Db |||||
Qy 541 TACAAATTTGAAGGACAGTGGAGGACTGATTTTCCCTCTCTCAATACATCTATGTT 600
Db |||||
Qy 569 TACGCAATTTGAAGACATAGTGGAGGACTTCTGTTCCTCTCTCTATGTGCTGTTGTT 628
Db |||||
Qy 601 ATGTCAAAATTAAGTGTCAAACTTTCATGAGAGGTTAAATAATATCATCTATGTG 660
Db |||||
Qy 629 ATGTCAAGAACTAAGTGACCAATGACTTTTCAAGAGGTTAAATAATATCATCTATGTG 688
Db |||||
Qy 661 CTTTATTTTGACTTTTGGTCCAAATGCTGATATGAAGAGTGGGATCAGTTTACAGT 720
Db |||||
Qy 689 CTTTATTTTGAATTTTGGTCCCAATATTTGACATGAAGAGTGGGATCAGTTTACAGT 748
Db |||||
Qy 721 GAAGTTTGAAGAACCCACTTACCTTATTTGAGACAATGGGAAAGCTGACATATGCTT 780
Db |||||
Qy 749 GAAGTTTGAAGAACCCACTTACCTTATCTGAGACAATGGGAAAGCTGACATATGCTT 808
Db |||||
Qy 781 ATCGAAACTCTCGAGTTTTCATTTTCCATCTTCTTACCAAGCTGATTTGTT 840
Db |||||
Qy 809 ATTGAAACTCTCGAGTTTTCATTTTCCCTCACCCTCTTACCAAGCTGATTTGTT 868
Db |||||
Qy 841 GGAGGATTTCCACTGCAAACTGCGCAAAACCCCTACTTAAGGAAATGGAGGAGTTGTACAG 900
Db |||||
Qy 869 GGAGGATTTCCACTGCAAACTGCGCAAAACCCCTACTTAAGGAAATGGAGGAGTTGTCCAG 928
Db |||||
Qy 901 AGCTCTGGAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
Db |||||
Qy 929 AGCTCTGGAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 988
Db |||||
Qy 961 GCAGAAAGGGCCAAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAGTTCTGTGG 1020
Db |||||
Qy 989 GAAGAAAGGGCCAAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAGTTCTGTGG 1048
Db |||||
Qy 1021 AGATTTGACGGGAATAAACAGATGCTTGGTCTCAATCTCGGCTGTACAAGTGGATA 1080
Db |||||
Qy 1049 AGATTTGATGGGAATAAACAGATGCTTGGTCTCAATCTCGGCTGTACAAGTGGATA 1108
Db |||||
Qy 1081 CCCAGAAATGACCTTCTAGTGTATCCAAAACCCAGAGCTTTTAACTCATGTGGAGCC 1140
Db |||||
Qy 1109 CCCAGAAATGATCTTCTTGGTCAACCAAAACCCAGAGCTTTTAACTCATGTGGAGCC 1168
Db |||||
Qy 1141 AATGGCATCTATGAGGCAATCTACCATGCGATCCCTATGTTGGGCACTTCCATGTTT 1200
Db |||||
Qy 1169 AATGGCATCTATGAGGCAATCTACCATGCGATCCCTATGTTGGGCGTTCATGTTTGGCA 1228
Db |||||
Qy 1201 GATCAACTGATTAACATTTGCTCAGATGAAGGCGGAGGAGCTGTTAGATGGAGCTTC 1260
Db |||||
Qy 1229 GATCAACTGATTAACATTTGCTCAGATGAAGGCGGAGGAGCTGTTAGATGGAGCTTC 1288
Db |||||
Qy 1261 AACCAATGTCAGTACAGACCTGCTCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1320
Db |||||
Qy 1289 CACAATGTCAGTACAGACCTTACTCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1348
Db |||||
Qy 1321 TATAAGAGAAATATTAATGAATTAATGAATTAATGAATTAATGAATTAATGAATTAATGAATTAAT 1380
Db |||||
Qy 1349 TATAAGAGAAATGCTATGAATTAATGAATTAATGAATTAATGAATTAATGAATTAATGAATTAAT 1408
Db |||||

RESULT 7

US-09-949-016-3181
; Sequence 3181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3181
; LENGTH: 2092
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3181

Query Match 79.6%; Score 1370, 8; DB 4; Length 2092;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 192; Indels 6; Gaps 3;

Qy 1 TGCACAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTATC 60
Db 29 TGCATCAGGATGCTATGAATGGACTTCAGTTCTTCTGCTGATACATCAGTTGTATC 88
Qy 61 TTTAGCTCTGGAGTTGTGGAAAGTGTCTGGTGTGGCCCGCAGAAATACAGCCATTTGGATG 120
Db 89 TTTAGCTCTGGAGTTGTGGAAAGTGTCTGGTGTGGCCCGCAGAAATTCAGCCACTGGATG 148
Qy 121 AATATGAGACATCTGTAAGAGCTTGTTCAGAGAGTGTTCAGAGAGTGTTCAGAGTGTTCAG 180
Db 149 AATATAAGACATCTGTAAGAGTGTTCAGAGAGTGTTCAGAGAGTGTTCAGAGTGTTCAG 208
Qy 181 TCTTACGCTTCCATTTCTTTTGTATCCCAATGATGCTCCACTCTCTTAATTTTGAAGTTAT 240
Db 209 TCTTACGCTTCCATTTCTTTTGTATCCCAATGATGCTCCACTCTCTTAATTTTGAAGTTAT 268
Qy 241 CTTACATCTTTAATACTAAACTGAAATTTGAGAAATATCATATGCAACAGGTTTAAGAGATGG 300
Db 269 CTTGATCTTTAATACTAAACTGAAATTTGAGAAATATCATATGCAACAGGTTTGGTAAAGATGG 328


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Qy 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATATTTTTCACAGAACCAAGAAATCCCTGTGG 360
Db 329 GCAGAACTTCACAAAGACACATTTTGGTCATATTTTTCACAGATACAGAAATCATGTGG 388
Qy 361 GAATATATGACATATTTAGAACTCTCTGAAAGATAGTTTCAAATAAGAAAGTTATG 420
Db 389 ACATTTAATGACATATCTAGAAAGTCTGTAAGGATATAGTTTCAAATAAGAAATTTATG 448
Qy 421 AAAAACTACAGAGTCAAGATTTGACATCGTTTTCAGATGCTGTTTTCCTGTGGT 480
Db 449 AAAAACTACAGAGTCAAGATTTGATGTTTCTTCAGATGCTGTTTTCCTGTGGT 508
Qy 481 GAGCTGCTGGCTGGCTTAACTAAACATACGGTTTGTGACAGTCTCCGCTTTACTTCCCTGGC 540
Db 509 GAGCTGCTGGCGAGTTACTTAAATACCTTTGTCTACAGGCTCGCTTCTCTCTGGC 568
Qy 541 TACAAATTTAAAGGACAGTGGAGGACTGATTTTCCCTCTCTCTACATACCTATTTGTT 600
Db 569 TACCAATTTAAAGACATAGTGGAGGACTTCTGTTCCTCTCTCTCTATGTGCTGTTGTT 628
Qy 601 ATGTCAAAATTAAGTGATCAAACTTTTATGAGAGGCTTAAATAATATGATCTATGTG 660
Db 629 ATGTCAAACTTAAGTGACCAATGACTTTTCATAGAGAGGCTTAAATAATATGATCTATGTG 688
Qy 661 CTTTATTTTGACTTTTGGTTCCAAATGCTGATATGAAGAAGTGGATCAGTTTTCACAGT 720
Db 689 CTTTATTTTGAATTTTGGTTCCAAATATTTGACATGAAGAAGTGGATCAGTTTTCACAGT 748
Qy 721 GAAGTTTGTAGGAAGACCCACTACCTTATTTGAGCAATGGGAAAGCTGACATATGGCTT 780
Db 749 GAAGTTCTAGGAAGACCCACTACCTTATCTGAGCAATGGCAAAAGCTGACATATGGCTT 808
Qy 781 ATGCAAACTCTGGAGTTTTCATTTTCTCTCATCTCTTACCAACGTTGATTTGTT 840
Db 809 ATTGCAAACTACTGGGATTTTCAATTTTCTCACCCCTCTTTACCAAAATGTTGAGTTGCTT 868
Qy 841 GGAGGATTTCAACTGCAAACTGCAAACTCTTAAAGAAATGGAGGAGTTTGTACAG 900
Db 869 GGAGGATCTCACTGCAAACTGCAAACTCTTAAAGAAATGGAGGAGTTTGTCCAG 928
Qy 901 AGCTCTGGAGAAATAGTGTGTGGTGTCTTCTGGGGTCAAGTAAAGTAAACATGACA 960
Db 929 AGCTCTGGAGAAATAGTGTGTGGTGTCTTCTGGGGTCAAGTAAAGTAAACATGACA 988
Qy 961 GCAGAAAGGCGCAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAGGTTCTGTG 1020
Db 989 GAAGAAAGGCGCAATGTAATTTGCAATCAGCCCTTCCCAAGATCCCAAAAGGTTCTGTG 1048
Qy 1021 AGATTTGACGGGAATAACACAGATGCTTAGTGTCTCAATCTCGGCTGTACAAGTGGATA 1080
Db 1049 AGATTTGATGGGAATAACACAGATCTTTAGGACTCAATCTCGGCTGTACAAGTGGATA 1108
Qy 1081 CCCAGAAATGACCTTCTAGGTGATCCAAAAACAGAGCTTTTAACTCATGTGGGAGCC 1140
Db 1109 CCCAGAAATGATCTTCTTGGTCACCCCAAAACAGAGCTTTTAACTCATGTGGGAGCC 1168
Qy 1141 AATGGCATCTAGGCAATCTACATGGGATCCCTATGTGGGCAATCCATGTTTGT 1200
Db 1169 AATGGCATCTAAGGCAATCTCTCTAGAAATCCCTATGTGGGCGTTTCCATGTTTGTGCA 1228
Qy 1201 GATCAACTGATAACATTTGCTACATGAAGCCCAAGGAGGAGCGTGTAGATTGGACTTC 1260
Db 1229 GATCAACTGATAACATTTGCAATGAAGCCCAAGGAGGAGCGTGTAGTTGGACTTC 1288
Qy 1261 AACCAATGTCCAGTACAGACCTCTGATGCACTGAAGACAGTAAATTAATGATCCTTTA 1320
Db 1289 CACCAATGTCCAGTACAGACCTTACTCAATGCACTGAAGACAGTAAATTAATGATCCTTTA 1348
Qy 1321 TATAAGAGAAATATATGAATTTATCAAGATTTCAATGATCAACAGTAAAGCCCTG 1380
Db 1349 TATAAGAGAAATGCTATGAATTTATCAAGATTTATCAATGATCAACAGTAAAGCCCTT 1408
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Qy 1381 GATCGAGCAGTCTTCTGGATTGAATTTGTATGCCCCCAAGAGGAGCAACACCTTCGA 1440
Db 1409 GATCGAGCAGTCTTCTGGATTGAATTTGTATGCCCCCAAGAGGAGCAACACCTTCGG 1468
Qy 1441 GTTGCAGCCCATGACCTCAGCTGGTTCCAGTACACACTCTTTGGATGTGATGGTTCTG 1500
Db 1469 GTTGCAGCCCATGACCTCAGCTGGTTCCAGTACACACTCTTTGGATGTGATGGTTCTG 1528
Qy 1501 CTGGCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTGTCTGTGTTTGTCTGG 1560
Db 1529 CTGGCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTGTCTGTGTTTGTCTGG 1588
Qy 1561 AAGTTTGTCTAGAAAGGAGAAAGAGGAAAGAGATTAGTTATGTCTGACATTTGAAAGCT 1620
Db 1586 AAGTTTGTCTAGAAAGGAGAAAGAGGAAAGAGATTAAATTTACGTCTGAGGCTGGAAGCT 1645
Qy 1621 GAAAACCATGATAGTAGGCAACTTCAGTTTATTCAGCAAGAAAGAAAGATTTGTTAT 1680
Db 1646 GAAAACCATGATAGTAGGCAACTTCAGTTTATTCAGCAAGAAAGAAAGATTTGTTAT 1702
Qy 1681 GCAAGATTTCTTCTCTCTCTGACAAAAAAGAAAAA 1720
Db 1703 AAGAGATTCCTTCTCTCTGACAAAAAAGAAAAA 1742

RESULT 9
US-09-180-852-1
; Sequence 1, Application US/09180852
; Patent No. 6287834
; GENERAL INFORMATION:
; APPLICANT: BELANGER, Alain
; APPLICANT: HUM, Dean W.
; APPLICANT: BEAULIEU, Martin
; APPLICANT: LEVESQUE, Eric
; TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE
; TITLE OF INVENTION: DIPOHOSHO-GLUCURONOSYLTRANSFERASE
; FILE REFERENCE: 1259-449
; CURRENT APPLICATION NUMBER: US/09/180,852
; CURRENT FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: PCT/CA97/00328
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: US 08/649,319
; EARLIER FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(1644)
US-09-180-852-1

Query Match 70.8%; Score 1219.2; DB 3; Length 2107;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1430; Conservative 0; Mismatches 268; Indels 10; Gaps 4;

Qy 4 ACAGGATGACTCTGAATGAGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTACTTT 63
Db 46 ACCAGGATGTCTGAAATGGATGTCAGTCTTCTGCTGATGCGAGCTCAGTTGTACTTT 105
Qy 64 AGCTCTGGGAGTTGTGAAAGAGTCTGCTGTGGCCGAGAAATACAGCAATGGATGAAT 123
Db 106 AGCTCTGGGAGTTGTGAAAGAGTCTGCTGTGGCCGAGAAATACAGCAATGGATGAAT 165
Qy 124 ATGAAGACAATCTCTGAAGAGCTTTGTTTCAGAGAGGTCAATGAGGTGACTGTACTGCACT 183
Db 166 ATGAAGACAATCTCTGAAGAGCTTTGTTTCAGAGAGGTCAATGAGGTGACTGTACTGCACT 225
Qy 184 TCAGCTTCCATCTTTTGTATCCCAATGATGATCCCACTCTTAATTTGAAGTTTATCCT 243
Db 226 TCGGCTTCTATTTCTTGTGTAATGCGCAAGTAAATCATCTGCTATTAATAGAAAGTTATCCT 285
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QY 244 ACATCTTTAACTAAACTGAATTTGAGATATCATCATGCAACAGGTTTAAGAGATGTC 303
Db 286 ACATCTTTAACTAAACTGAATTTGGAAGATTTTATGAAAAATGTTTCGATATGAC 345
QY 304 GA-- -CATTCGAAAGATAGCTTTTGGTTATATTTTTCACAAGAAACAAGAAATCCCTGTGG 360
Db 346 TATAGTATTTCAAAAAATACATTTTGGTCATATTTTTCACAACCTACAGAATTTGTGTGG 405
QY 361 GAATTTATGACATATTTAGAAAATCTCTGTAAGAATGTAGTTTCAATAAGAAAGTTATG 420
Db 406 GAATTTCTGACTATAATATAAAGCTCTGTGAAGATGCAGTTTGAACAAGAAATATG 465
QY 421 AAAAAACTACAAGATCAAGATTTGACATCGTTTTTTCAGATGCTGTTTTTCCCTGTGGT 480
Db 466 AGAAAACTACAAGATCAAAATTTGATGTCTTTCTGGCAGATCCGTTAACTCCCTGTGGT 525
QY 481 GAGCTGTGCTCGCTGCTTACATTAACATACGGTTTTGTGFACAGTCTCCGCTTTTACTCCTGGC 540
Db 526 GAGCTGTGCTGAACTACTTTAAACATACCCTTTCTGTACAGTCTCCGCTTTCTCTGTGGC 585
QY 541 TACACAATTTGAAAGGCACAGTGGAGGACTGAATTTTCCCTCTTCTCCTACATACCTATTGTT 600
Db 586 TACACAGTTTGAGAAGAAATGCTGGAGGATTTCTGTTCCTCTTCTCTATGTACCTGTGTT 645
QY 601 ATGTCAAAATTAAGTATGATCAAAATGACTTTTCATGAGAGGGTAAAAAATATGATCTATGG 660
Db 646 ATGTCAGAATTAAGTATGATCAAAATGATTTTCATGAGAGGATTAAAAAATATGATATATATG 705
QY 661 CTTTATTTTGACTTTTGGTTCCAAATGTCATGATGAAGAGTGGGATCAGTTTTCACAGT 720
Db 706 CTTTATTTTGACTTTTGGTTTCAAGCATATGATCTGAAGAGTGGGACCAAGTTTATAGT 765
QY 721 GAAGTTTATAGGAAGACCCACTACTCTTATTTGAGACAAATGGGAAAGCTGACATATGGCTT 780
Db 766 GAAGTTCTAGGAAGACCCACTACTATTTATTTGAGACAAATGGGAAAGCTGAAATGTGGCTC 825
QY 781 ATCGAAACTCTGGAGTTTCAATTTCCCTCATCCATTTTACCAACGTTGATTTGTT 840
Db 826 ATTCGAACCTATTGGGATTTTGAATTTCCCTCGCCCATCTTTACCAAAATGTTGATTTGTT 885
QY 841 GGAGGATTCACATGCAAACTCGCAAAACCCCTACCTAAGGAAATGGAGGAGTTGTACAG 900
Db 886 GGAGGACTTCACTGTAAACAGCCAAACCCCTTGCCCTAAGGAAATGGAGAGTTGTGTCAG 945
QY 901 AGCTCTGGAAAAATGGTGTGTGGTGTGTTTCTCTGGGTCAGTGATAAGTAACATGACA 960
Db 946 AGCTCTGGAAAAATGGTATTGTGGTGTGTTTCTCTGGGTCGATGATCAGTAACATGTCA 1005
QY 961 GCAGAAAGGCCCAATGTAATTTGCAACAGCCCTTGCCCAAGATCCCAAAAGTTCTGTGG 1020
Db 1006 GAAGAAAGTGCACCAATGATTTGATCAGCCCTTGCCCAAGATCCCAAAAGTTCTATGG 1065
QY 1021 AGATTTGACGGGAATAAACCCAGATGCTTAGGTCTCAATACTCGGCTGTACAAGTGGATA 1080
Db 1066 AGATTTGATGGCAAGAGCCAAATATTTTAGTTCCAAATCTCGACTGTATAAGTGGTTA 1125
QY 1081 CCCCAGAAATGACCTTCTAGTGTATCCAAAAACAGAGCTTTTATACTCATGTGTGAGCC 1140
Db 1126 CCCCAGAAATGACCTTCTTGGTATCCCAAAACCAAAGCTTTTATACTCATGTGTGAAACC 1185
QY 1141 AATGGCATCTATGAGGCAATCTACCATGGATCCCTATGTTGGGATTCCTATGTTTTTTT 1200
Db 1186 AATGGCATCTATGAGGCGATCTACCATGGATCCCTATGTTGGGATTCCTATGTTTTTGG 1245
QY 1201 GATCAACCTGATAAATTTGCTACATGAAGGCCCAAGGAGCAGCTGTAGATTTGGACTTC 1260
Db 1246 GATCAACATGATAACATTTGCTACATGAAGCCAAAGGAGCAGCCCTCAGTGTGGACATC 1305
QY 1261 AACACAATGTGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCTTTTA 1320
Db 1306 AGGACCATGTCAAGTAGAGATTTGCTCAATGCATTTGAAAGTCAGTCATTAATGACCCTATC 1365
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QY 1321 TATAAAGAGAATATTTATGAAATTTATCAAGAAATTTCAACATGATCAACACAGTAAAGCCCTG 1380
Db 1366 TATAAAGAGAATATCATGAAATTTATCAAGAAATTTATCATGATCAACCGGTGAAGCCCTG 1425
QY 1381 GATCGAGCAGTCTTCTGGATTTGAATTTGTTCATGCCCCCAAAAGAGGCCAAACACCTTCGA 1440
Db 1426 GATCGAGCAGTCTTCTGGATTTGAGTTTGTATGCGCCATTAAGGAGCCAAAGCACCTTCGG 1485
QY 1441 GTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTTCTG 1500
Db 1486 GTCGCAGCCCAACACCTCACCTGGATCCAGTACCACCTCTTTGGATGTGATAGCATTCCTG 1545
QY 1501 CTGGCCTGTGTGGCACTGTGATATTTATCATCAAAAGTTTGTCTGTTTGTCTGTTCTGG 1560
Db 1546 CTGGCCTGTGTGGCACTGTGATATTTATGATCAGAAATGTTTGCCTGTTTGTTCGGA 1605
QY 1561 AAGTTTGTAGAAAAGGGGAAGGAAAGGAAAAGAGATTAGTTATGTCTGACATTTGAAGCT 1620
Db 1606 AAGCTTGCCAAACACAGGAAGAAAGAAAGAGATTAGTTATCAAAAGCCTGAAG-T 1664
QY 1621 GGAAAACCCAGATAGATAGGACAACTTCAGTTTATTTCCAGCAAGAAAAGAAAGATTGTTAT 1680
Db 1665 GGAATGACCAAAAGATGGGACTCCTCC--TTTATTCCAGCATGGAG---GTTTTAAAT 1718
QY 1681 GCNAGATTTTCTTCTTCTCTGTGACAAAA 1708
Db 1719 GGAGGATTTTCTTCTTCTCTGCGACAAAA 1746

RESULT 10
US-09-356-806-112
; Sequence 112, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and
; TITLE OF INVENTION: 2B15 (UGT2B15) Genes
; FILE REFERENCE: SEQ-22PRV2
; CURRENT APPLICATION NUMBER: US/09/356,806
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 1976
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)...(1598)
US-09-356-806-112

Query Match 70.5%; Score 1213.6; DB 4; Length 1976;
Best Local Similarity 83.1%; Pred. No. 0;
Matches 1421; Conservative 0; Mismatches 279; Indels 10; Gaps 3;

QY 4 ACCAGGATCAGCTCTGAAATGGACTTCAGTTCTTCTCTGATACATCTCAGTTCTGTTACTTTT 63
Db 5 ACCAGATCTCTCTGAAATGGAGCTCAGTCTTCTGCTGATACAGCTCAGTTGTTACTTTT 64
QY 64 AGCTCTGGAGTTGTGGAAAAAGTGTGGTGTGGGCCGACAGAAATACAGCCATTGGATGAAT 123
Db 65 AGCTCTGGAAAGCTGTGGAAAGGTGCTAGTGTGGCCACAGAAATACAGCCATTGGATAAAT 124
QY 124 ATCAAGACAAATCCTGAAAGAGCTTGTTCAGAGAGGTCAAGTGAAGTCTGACTGCTGATCT 183
Db 125 ATGAAGACAAATCCTGGAAGAGCTTGTTCAGAGGGGTCAAGTGAAGTCTGTTGTCATCT 184
QY 184 TCAGCTTCCATCTCTTTTTCATCCCAATGATGCATCCACTCTTTAAATTTGAAGTTTATCCT 243
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Db 185 TCGGCTTCTACTCTTTGTCATGCGCAGTAAATCATCTGCTATTAATAATTAGAGTTTATCCT 244
Qy 244 ACATCTTTAACTAAACCTGAATTTTGAGAAATATCATCATGCAACAGGTTTAAGAGATGG--- 300
Db 245 ACATCTTTAACTAAATGATTTTGAAGATTTCTCTTCTGAAAAATCTCGATAGATGATA 304
Qy 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAAGAAATCCTGTGG 360
Db 305 TATGGTGTTCAAAAAATACATTTTGGTCAATTTTTCACAATTTACAAAGAAATTTGTGTGG 364
Qy 361 GAAATATATGACATATTTAGAACTTCTGTGAAGATGAGTTTCAATATAAGAAAGTTATG 420
Db 365 GAAATATATGACTACAGTAACAAAGCTCTGTGAAGATGCAAGTTTTTGAATAAGAAATTTATG 424
Qy 421 AAAAAAATACAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTGTTCCTCCCTGGGT 480
Db 425 ATGAACCTACAGAGTCAAAGTTTGTATGTCATTTCTGCGAGATGCCCTTAATCCCTGGGT 484
Qy 481 GAGCTGTGGCTGGCTACTTTAAACATACGGTTTGTGTACAGTCTCCGCTTTACTCTGGC 540
Db 485 GAGCTACTGGCTGAACATATTTAAACATACCCCTTCTGTACAGTCTTCGATTCTCTGTGGC 544
Qy 541 TACACAATTTGAAGGCACAGTGGAGGACTGATTTTCCCTCTCTACATACCTATTGTT 600
Db 545 TACACATTTGAGAGAAATGGTGGAGGATTTCTGTTCCTCTCTATGATACCTGTTGTT 604
Qy 601 ATGTCAAAATTAAGTATCAAAATGACATTTTCATGAGAGGGTAAATAATATGATCATGTG 660
Db 605 ATGTCAAGATTAAGTATCAAAATGATTTTCATGAGAGGATTAATAATATGATACATATG 664
Qy 661 CTTTATTTTGAATTTGTTGCCAATGTCATATGAAGAGTGGGATCAGTTTTTACAGT 720
Db 665 CTTTATTTTGAATTTGTTGCCAATGTCATATGAAGAGTGGGATCAGTTTTTATAGT 724
Qy 721 GAAGTTTGAAGAACCACTACTTATTTGAGACAATGGGAAAGCTGACATATGCGTT 780
Db 725 GAAGTTTGAAGAACCACTACTTATTTGAGACAATGGGAAAGCTGAAATGTCGCT 784
Qy 781 ATGCGAACTCTCGAGTTTTCAATTTCTCTCATCATCTTTTACCACAAAGTTGATTTGTT 840
Db 785 ATTGGAACCTATTGGGATTTTGAATTTTCTCTGCCCATCTTTACCACAAATGTTGATTTGTT 844
Qy 841 GGAGGATTTCACTGCAACCTGCCAAACCCCTACTTAAGGAAATGGAGGATTTGTACAG 900
Db 845 GGAGGATTTCACTGTAACCAAGCAACCCCTGCTTAAGGAAATGGAGGATTTGTGAG 904
Qy 901 AGCTCTGGAGAAATAGTGTGTGGTGTGTTCTCTGGGTCAGTGAATGAATACATGACA 960
Db 905 AGCTCTGGAGAAATAGTGTGTGGTGTGTTCTCTGGGTCAGTGAATGAATACATGACA 964
Qy 961 GCAGAAAGGGCCAAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAAGGTTCTGTGG 1020
Db 965 GAAGAAAGTGCACATGATTTGATTCAGCCCTTCCCAAGATCCCAAAAAGGTTCTATGG 1024
Qy 1021 AGATTTGACGGGAATAAACACAGATGCTTAGGTCTCAATATCTCGGCTGTACAAGTGATA 1080
Db 1025 AGATTTGATGCAAGAACCAAAATACTTTAGTTTCCAATCTCGACTGTACAAGTGATA 1084
Qy 1081 CCCAGAAATGACCTTTAGTTCATCCAAAACAGAGCTTTTATACTCATGTGTGGAGCC 1140
Db 1085 CCCAGAAATGACCTTTTGGTTCATCCAAAACCAAGCTTTTATACTCATGTGTGGAGCC 1144
Qy 1141 AATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGTGGGCAATTCATATGTTTTTT 1200
Db 1145 AATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGTGGGCAATTCCTCTGTTGGC 1204
Qy 1201 GATCAACCTGATAACATTTGCTCACATGAAGGCCAAGGAGCAGCTGTTAGATTCGACTTC 1260
Db 1205 GATCAACATGATAACATTTGCTCACATGAAGGCCAAGGAGCAGCCCTCAGTGTGACATC 1264
Qy 1261 AACCAATGTGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTTTA 1320
Db 1265 AGGACCATGTCAAGTAGAGATTTGCTCAATGCAATGAAGTCAGTCAATTAATGACCCCTGTC 1324
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Qy 1321 TATAAAGAGAAATATTATGAAATTTATCAAGAAATTCACAATGATCAACAGTAAGCCCTG 1380
Db 1325 TATAAAGAGAAATGTCATGAAATTTATCAAGAAATTCATGACCAACCAATGAGCCCTG 1384
Qy 1381 GATCGAGCAGCTCTTCGTGATTTGAAATTTGTATGCCCCACAAAGAGGCCAAACACCTTGA 1440
Db 1385 GATCGAGCAGCTCTTCGTGATTTGAAATTTGTATGCCCCACAAAGAGGCCAAACACCTTGA 1444
Qy 1441 GTTCGAGCCCATGACCTCAGCTGTTCCAGTACCACCTTTTGGATGATGATTTGGCTTTCTG 1500
Db 1445 GTTCGAGCTCACACCTCAGCTGATCCAGTACCACCTTTTGGATGATGATGATTCCTG 1504
Qy 1501 CTGCGCTGTGTGGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTTTTGTTTCTG 1560
Db 1505 CTGCGCTGTGTGGCAACTGTGATATTTATCATCAAAATTTTGCCTGTTTGTTCGA 1564
Qy 1561 AAGTTTGTCTAGAAAAGGAAAGAGGAAAGAGATTAGTTATGCTGTGACATTTGAAGCT 1620
Db 1565 AAGTTTGTCTAGAAAAGGAAAGAGGAAAGAGATTAGTTATATCAAAAGCCTGAAG-T 1623
Qy 1621 GGAACCACGATAGATAGGACAACTTCAGTTTATTCAGCAAGAAAGAAAGATTTGTTAT 1680
Db 1624 GGAATGACTCAAAAGATGGGACTCCTCTCTTATTTT-----CAGCATGGAGGTTTAAAT 1677
Qy 1681 GCAAGATTTCTTCTCTCTCTGACAAAAA 1710
Db 1678 GGAGGATTTCTTTTCTCTGACAAAAA 1707
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RESULT 11

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US-09-813-918-1
; Sequence 1, Application US/09813918
; General Information:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001175
; CURRENT APPLICATION NUMBER: US/09/813,918
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Human
US-09-813-918-1
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Query Match 66.9%; Score 1151.8; DB 3; Length 1413;

Best Local Similarity 85.7%; Pred. No. 0;

Matches 1391; Conservative 0; Mismatches 7; Indels 225; Gaps 1;

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Qy 1 TGCACACAGGATGACTCTGAAATGGACTTCAGTTCTCTCTGTGATACATCTCAGTTGTTAC 60
Db 14 TGCACACAGGATGACTCTGAAATGGACTTCAGTTCTCTCTGTGATACATCTCAGTTGTTAC 73
Qy 61 TTTAGCTCTGGGAGTTGTGAAAAAGTCTCGTGTGGCCCGCAGAAATACAGCCATTGGATG 120
Db 74 TTTAGCTCTGGGAGTTGTGAAAAAGTCTCGTGTGGCCCGCAGAAATACAGCCATTGGATG 133
Qy 121 AATATGAAGCAATCTCTGAAAGAGCTTGTTCAGAGAGTTCATGAGGTGACTGTACTGGCA 180
Db 134 AATATGAAGCAATCTCTGAAAGAGCTTGTTCAGAGAGTTCATGAGGTGACTGTACTGGCA 193
Qy 181 TCTTCAGTCTCCATCTCTTTTGTATCCCAATGATGCTCCACTCTTAAATTTGAAGTTTAT 240
Db 194 TCTTCAGTCTCCATCTCTTTTGTATCCCAATGATGCTCCACTCTTAAATTTGAAGTTTAT 253
Qy 241 CCTACATCTTTAACTAAAACCTGAAATTTGAGAATATCATATGCAACAGGTTTAAGAGATGG 300
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Db 254 CCTACATCTTTAACTAAAAGTGAATTTGAGATATCATCATGCAACAGGTTAAGATGG 313
QY 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAGAAACAAGAAATCCCTGTGG 360
Db 314 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAGAAACAAGAAATCCCTGTGG 373
QY 361 GAATATATGACATATTTAGAACTTCTGTAAAGATGATGTTTCAATAGAAAGTTATG 420
Db 374 GAATATATGACATATTTAGAACTTCTGTAAAGATGATGTTTCAATAGAAAGTTATG 433
QY 421 AAAAACTACAAGATCAAGATTTGACATCGTTTTTTCAGATGCTGTTTTTCCCTGTGGT 480
Db 434 AAAAACTACAAGATTTAGATTTGACATCGTTTTTTCAGATGCTGTTTTTCCCTGTGGT 493
QY 481 GAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCGCTTTACTCTCGGC 540
Db 494 GAGCTGCTGGCTGCGCTACTTAACATAC----- 521
QY 541 TACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGTT 600
Db 522 ----- 521
QY 601 ATGTCAAAATTAAGTGTATCAAAATGACTTTTCATGGAGAGGTAAAAAATATGATCTATGTG 660
Db 522 ----- 521
QY 661 CTTTATTTTGACTTTTGGTTTCCAAATGTCGTGATATGAAGAAGTGGGATCAGTTTACAGT 720
Db 522 ----- 521
QY 721 GAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGRAAAGCTGACATATGCTTT 780
Db 522 -----GACCCACTACCTTATTTGAGACAATGGRAAAGCTGACATATGCTTT 568
QY 781 ATGCGAAATCCTCGAGTTTTCAATTTCCCTCATCCATTTCTTACCAACGTTGATTTGTT 840
Db 569 ATGCGAAACCCCTGGAGTTTCAATTTCCCTCATCCATTTCTTACCAACGTTGATTTGTT 828
QY 841 GGAGGATTCACATGCAAAACCTGCAAAACCCCTACCTTAAGCAATGGAGAGTTGTACAG 900
Db 629 GGAGGATTCACATGCAAAACCTGCAAAACCCCTACCTTAAGCAATGGAGGAGTTGTACAG 688
QY 901 AGCTCTGGAGAAATAGTGTGTGGTGTCTCTCGGGTCACTGATAGTAACATACATGACA 960
Db 689 AGCTCTGGAGAAATAGTGTGTGGTGTCTCTCGGGTCACTGATAGTAACATACATGACA 748
QY 961 GCAGAAAGGCCCAATGTAATTTGCAACAGCCCTTTGCCAAGATCCCAAAAAGTTCTGTGG 1020
Db 749 GCAGAAAGGCCCAATGTAATTTGCAACAGCCCTTTGCCAAGATCCCAAAAAGTTCTGTGG 808
QY 1021 AGATTTGACGGGAATTAACACAGATGCTTTAGGTCTCAATACTCGGCTGTACAAGTGGATA 1080
Db 809 AGATTTGACGGGAATTAACACAGATGCTTTAGGTCTCAATACTCGGCTGTACAAGTGGATA 868
QY 1081 CCCAGAAATGACCTTCTAGTGTATCAAAAACAGAGCTTTTATAACTCATGTGTGGAGCC 1140
Db 869 CCCAGAAATGACCTTCTAGTGTATCAAAAACAGAGCTTTTATAACTCATGTGTGGAGCC 928
QY 1141 AATGGCATCTATGAGGCAATCTAACATGGGATCCCTATGTGGGCAATCCATTTGTTTTTT 1200
Db 929 AATGGCATCTATGAGGCAATCTAACATGGGATCCCTATGTGGGCAATCCATTTGTTTTTT 988
QY 1201 GATCAACCTGATTAACATTTGCTACATGAAGGCCAAGGGAGCAGCTGTAGATTGGACTTC 1260
Db 989 GATCAACCTGATTAACATTTGCTACATGAAGGCCAAGGGAGCAGCTGTAGATTGGACTTC 1048
QY 1261 AACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAAATTAATGATCCTTTA 1320
Db 1049 AACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAAATTAATGATCCTTTA 1108
QY 1321 TATAAAGAGAATATTTAGAAATTTATCAAGAAATTTCAACATGATCAACAGGTAAGCCCTG 1380
Db 1109 TATAAAGAGAATATTTAGAAATTTATCAAGAAATTTCAACATGATCAACAGGTAAGCCCTG 1168

RESULT 12

US-10-060-311-1

; Sequence 1, Application US/10060311

; Patent No. 6713295

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al.

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF

; FILE REFERENCE: CL001175DIV

; CURRENT APPLICATION NUMBER: US/10/060,311

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1413

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-060-311-1

Query Match 66.9%; Score 1151.8; DB 4; Length 1413;

Best Local Similarity 85.7%; Pred No. 0;

Matches 1391; Conservative 0; Mismatches 7; Indels 225; Gaps 1;

QY 1 TGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTTAC 60

Db 14 TGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTTAC 73

QY 61 TTTAGCTCTGGAGTTGTGGAAAAGTGTGGTGTGGGCCGCGAGAAATACAGCCATTGGATG 120

Db 74 TTTAGCTCTGGAGTTGTGGAAAAGTGTGGTGTGGGCCGCGAGAAATACAGCCATTGGATG 133

QY 121 AATATGAAGACAAATCCTGAAAGAGCTTTGTCAGAGAGTTCATGAGGTGACTGTACTGGCA 180

Db 134 AATATGAAGACAAATCCTGAAAGAGCTTTGTCAGAGAGTTCATGAGGTGACTGTACTGGCA 193

QY 181 TCTTCAGCTTCCATTTCTTTTGTGATCCCAATGATGCCATCCACTCTTAAATTTGAAGTTAT 240

Db 194 TCTTCAGCTTCCATTTCTTTTGTGATCCCAATGATGCCATCCACTCTTAAATTTGAAGTTAT 253

QY 241 CCTACATCTTTAACTAAAACCTGAAATTTGAGATATCATCATGCAACAGGTTAAGAGATCG 300

Db 254 CCTACATCTTTAACTAAAACCTGAAATTTGAGATATCATCATGCAACAGGTTAAGAGATCG 313

QY 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAGAAACAAGAAATCCCTGTGG 360

Db 314 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAGAAACAAGAAATCCCTGTGG 373

QY 361 GAATATATGACATATTTAGAAAACCTTCTGTAAGATGTAAGTTTCAATAAGAAAGTTATG 420

Db 374 GAATATATGACATATTTAGAAAACCTTCTGTAAGATGTAAGTTTCAATAAGAAAGTTATG 433

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Qy 421 AAAAACTCAAGAGTCAAGATTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGCGT 480
Db 434 AAAAACTCAAGAGTAAAGATTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGCGT 493
Qy 481 GAGCTGCTGGCTGGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTTACTCCTGGC 540
Db 494 GAGCTGCTGGCTGGCTACTTAACATAC----- 521
Qy 541 TACACAATTGAAGAGCAGTGGAGGACTGATTTTCCCTCCTTCTACATACCTATTGTT 600
Db 522 ----- 521
Qy 601 ATGTCAAAATTAAGTGATCAAAATGACTTTTATGAGAGGGGTAAATAATATGATCTATGT 660
Db 522 ----- 521
Qy 661 CTTTATTTTGACTTTTGGTCCAAATGTCTGATGAAGAAGTGGGATCAGTTTTTACAGT 720
Db 522 ----- 521
Qy 721 GAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAGCTGACATATGCGTT 780
Db 522 -----GACCCACTACCTTATTTGAGACAATGGGAAAGCTGACATATGCGTT 568
Qy 781 ATGCGAAACTCCTGGAGTTTTCAATTTTCCCTCATCTTCTTACCAACGTTGATTTTGT 840
Db 569 ATGCGAAACCCCTGGAGTTTTCAATTTTCCCTCATCTTCTTACCAACGTTGATTTGT 628
Qy 841 GGAGGATTCACCTCAAACTGCCAAACCCCTACTAAGGAAATGGAGGAGTTGTACAG 900
Db 629 GGAGGATTCACCTCAAACTGCCAAACCCCTACTAAGGAAATGGAGGAGTTGTACAG 688
Qy 901 AGCTCTCGAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
Db 689 AGCTCTCGAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748
Qy 961 GCAGAAAGGGCCAAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAAGTTCTGTGG 1020
Db 749 GCAGAAAGGGCCAAATGTAATTTGCAACAGCCCTTCCCAAGATCCCAAAAAGTTCTGTGG 808
Qy 1021 AGATTTGACGGGAATAAACGATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
Db 809 AGATTTGACGGGAATAAACGATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 868
Qy 1081 CCCAGAAATGACCTTCTAGGTGATCCAAACAGAGCTTTTAACTCATGTGTGGAGCC 1140
Db 869 CCCAGAAATGACCTTCTAGGTGATCCAAACAGAGCTTTTAACTCATGTGTGGAGCC 928
Qy 1141 AATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGTGGGCATTTCCATTGTTTTTT 1200
Db 929 AATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGTGGGCATTTCCATTGTTTTTT 988
Qy 1201 GATCAACCTGTATAACATTTGCTCAATGAAGCCCAAGGGAGCAGCTGTAGATGGAATTC 1260
Db 989 GATCAACCTGTATAACATTTGCTCAATGAAGCCCAAGGGAGCAGCTGTAGATGGAATTC 1048
Qy 1261 AACCAATGTGAGTACAGACCTCTGATGCACTGAAGACAGTAATTAATGATCCTTTA 1320
Db 1049 AACCAATGTGAGTACAGACCTCTGATGCACTGAAGACAGTAATTAATGATCCTTTA 1108
Qy 1321 TATAAGAGAAATATATGAATTTAAGAAATTCACATGATCAACAGTAAAGCCCTG 1380
Db 1109 TATAAGAGAAATATATGAATTTAAGAAATTCACATGATCAACAGTAAAGCCCTG 1168
Qy 1381 GATCGAGAGTCTTCTGGATTGAATTTGTCAATGCCCAAGAGGAGGCAACACCTTCGA 1440
Db 1169 GATCGAGAGTCTTCTGGATTGAATTTGTCAATGCCCAAGAGGAGGCAACACCTTCGA 1228
Qy 1441 GTTCAGCCCAATGACCTCAGCTGTTCCAGTACCACTCTTTTGGATGTGATTTGGTTCTG 1500
Db 1229 GTTCAGCCCAATGACCTCAGCTGTTCCAGTACCACTCTTTTGGATGTGATTTGGTTCTG 1288

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Qy 1501 CTGCGCTGTGTGGCACTGTGATATTATCATCAAAAGTTTTTGTCTGTTTTTGTCTGG 1560
Db 1289 CTGCGCTGTGTGGCACTGTGATATTATCATCAAAAGTTTTTGTCTGTTTTTGTCTGG 1348
Qy 1561 AAGTTTCTAGAAAAGGGAAAGGAAAGAGATTAGTTATGCTGTGACATTTTGAAGCT 1620
Db 1349 AAGTTTCTAGAAAAGGGAAAGGAAAGAGATTAGTTATGCTGCCACATTTTGAAGCT 1408
Qy 1621 GGA 1623
Db 1409 GAA 1411

RESULT 13
US-09-949-016-2735
; Sequence 2735, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2735
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2735

Query Match 55.9%; Score 962.2; DB 4; Length 1323;
Best Local Similarity 83.6%; Pred. No. 8, Re-268;
Matches 1103; Conservative 0; Mismatches 213; Indels 3; Gaps 1;

Qy 4 ACCAGGATGACTCTGAAATGAGCTTTCAGTTCTTCTGTGTATACATCTCAGTTGTACTTTT 63
Db 5 ACCAGGATGCTCTGAAATGAGCTGCTCTTCTGTGTATACATCTCAGTTGTACTTTT 64
Qy 64 AGCTCTGGGAGTTGTGGAAAAGTCTGCTGTGGGCCCCAGAAATACAGCCATTTGATGAT 123
Db 65 AGCTCTGGAAAGCTGTGGAAAAGTCTAGTGTGGCCCCACAGAAATACAGCCATTTGATGAT 124
Qy 124 ATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGCGCATCT 183
Db 125 ATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGCGCATCT 184
Qy 184 TCAGCTTCCATCTTTTGTATCCCAATGATGCAATCCATCTTAAATTTGAAGTTTATCCT 243
Db 185 TCAGCTTCTACTCTTGTCAATGCCAGTAAATCATCTGCTATTAATTTAGAAATTTATCCT 244
Qy 244 ACATCTTTAATAAAGTGAATTTGAGAATATCATCATGCAACAGGTTNAGAGATG--- 300
Db 245 ACATCTTTAATAAAGTGAATTTTGGAAAGTCTCTCTCGAAAATTCCTGATAGATGGATA 304
Qy 301 TCAGACAATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAAACAAGAAATCCTGTGG 360
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Db 665 CTTTATTTTGACTTTTGGTTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 724
QY 721 GAAGTTTGTAGGAAGACCCACTACCTTATTTTGACAAATGGGAAAGCTGACATATGGCTT 780
Db 725 GAAGTTTGTAGGAAGACCCACTACCTTATTTTGACAAATGGGAAAGCTGAAATGTGGCTC 784
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; Sequence 2736, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2736
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2736
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Best Local Similarity 83.6%; Pred. No. 8,8e-268;
Matches 1103; Conservative 0; Mismatches 213; Indels 3; Gaps 1;

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US-09-976-594-241
; Sequence 241, Application US/09976594
; Parent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 241
; LENGTH: 2966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 997080.1
US-09-976-594-241

Query Match 43.8%; Score 754.8; DB 4; Length 2966;
Best Local Similarity 67.8%; Pred. No. 1.4e-207;
Matches 1088; Conservative 0; Mismatches 507; Indels 9; Gaps 2;

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DB 143 TGTCAAGGTCTATCTAGAAGAGCTCATAGTCAGAGGCGCATGAGGTAAACAGTATTGACTCA 202
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QY 243 TACATCTTTAACTAAAACTGAATTTGAGAATAATCATCATGCAACAGGTTAGAGATGCTC 302
DB 263 TATGCCACAGCAGACAGAGAAATGAATAATTTTGTGACCTAGCTCTGA-----A 316
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GenCore version 5.1.6
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Searched: 9772377 seqs, 4126317084 residues

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Minimum DB seq length: 0

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Maximum Match 100%

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- 28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1693	98.3	1712	15	US-10-158-646-42
3	1584.2	92.0	2844	15	US-10-198-846-13134
4	1481.2	86.0	1855	9	US-09-880-107-2120
5	1481.2	86.0	1855	11	US-09-968-007A-368

6	1481.2	86.0	1855	11	US-09-968-007A-735	Sequence 735, App
7	1481.2	86.0	1855	21	US-10-783-528-57	Sequence 57, Appl
8	1481.2	86.0	1855	22	US-10-843-641A-6838	Sequence 6838, Ap
9	1481.2	86.0	1855	22	US-10-843-641A-7205	Sequence 7205, Ap
10	1481.2	86.0	1991	15	US-10-057-834A-1	Sequence 1, Appli
11	1478.6	85.9	2799	9	US-09-880-107-3756	Sequence 3756, Ap
12	1478.6	85.9	1854	15	US-10-205-522-39	Sequence 39, Appl
13	1454.6	84.5	1714	9	US-09-981-353-193	Sequence 193, App
14	1452.8	84.4	2802	24	US-10-450-763-5515	Sequence 5515, Ap
15	1436	83.4	1859	24	US-10-450-763-5514	Sequence 5514, Ap
16	1396	81.1	1639	19	US-10-468-125-18	Sequence 18, Appl
17	1375.6	79.9	2092	15	US-10-203-522-7	Sequence 7, Appli
18	1364.4	79.2	2093	9	US-09-880-107-3842	Sequence 3842, Ap
19	1361.4	79.1	2111	24	US-10-450-763-5516	Sequence 5516, Ap
20	1213.6	70.5	1976	15	US-10-205-522-112	Sequence 112, App
21	1213.6	70.5	2090	9	US-09-880-107-3292	Sequence 3292, Ap
22	1212	70.4	1829	17	US-10-252-157-24	Sequence 24, Appl
23	1198.8	69.6	2150	9	US-09-981-353-45	Sequence 45, Appl
24	1198.8	69.6	2150	17	US-10-252-157-25	Sequence 25, Appl
25	1175	68.2	2123	9	US-09-880-107-3285	Sequence 3285, Ap
26	1167.6	67.8	1816	24	US-10-491-183-62	Sequence 62, Appl
27	1157.8	66.9	1413	14	US-10-060-311-1	Sequence 1, Appli
28	1151.8	66.9	1413	20	US-10-778-300-1	Sequence 1, Appli
29	1151.8	66.9	1413	26	US-11-013-907-1	Sequence 1, Appli
30	1096.2	63.7	1614	19	US-10-381-898-24	Sequence 24, Appl
31	1027.8	59.7	1662	19	US-10-307-817-117	Sequence 117, App
32	1013.6	58.9	1608	22	US-10-498-788-57	Sequence 57, Appl
33	980.2	56.9	1356	24	US-10-491-183-98	Sequence 98, Appl
34	966.4	56.1	2573	22	US-10-764-420-2410	Sequence 2410, Ap
35	961	55.8	1961	9	US-09-917-800A-1403	Sequence 1403, Ap
36	949	55.1	1606	18	US-10-042-865-27	Sequence 27, Appl
37	949	55.1	1606	19	US-10-072-012-151	Sequence 151, Appl
38	895.4	52.0	1844	15	US-10-175-523-59	Sequence 59, Appl
39	895.4	52.0	1844	26	US-11-099-266-59	Sequence 59, Appl
40	856.2	49.7	1947	19	US-10-152-319A-2121	Sequence 2121, Ap
41	856.2	49.7	1947	22	US-10-486-706-279	Sequence 279, App
42	853.4	49.6	2634	18	US-10-388-934-169	Sequence 169, App
43	849	49.3	1593	19	US-10-152-319A-1908	Sequence 1908, Ap
44	805	46.7	1224	19	US-10-381-898-32	Sequence 32, Appl
45	765.2	44.4	1756	16	US-10-235-994-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-981-353-189
; Sequence 189, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 189
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 480489.5
US-09-981-353-189

Query Match 98.3%; Score 1693; DB 9; Length 1712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 248 CCTACATCTTTAACTAAACTGAATTTGAGATATCATCATGCAACAGGTGTAAGAGATGG 307
QY 301 TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAGAAACAAGAAATCCCTGTGG 360
Db 308 TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAGAAACAAGAAATCCCTGTGG 367
QY 361 GAATTTATGACATATTTAGAAACTTCTGTAAGATGTAGTTTCAAATTAAGAAAGTTATG 420
Db 368 GAATTTATGACATATTTAGAAACTTCTGTAAGATGTAGTTTCAAATTAAGAAAGTTATG 427
QY 421 AAAAACTACAGAGTCAGATTTGACATCGTTTTTGCAGATGCTGTTTTCCCTGTGT 480
Db 428 AAAAACTACAGAGTCAGATTTGACATCGTTTTTGCAGATGCTGTTTTCCCTGTGT 487
QY 481 GAGCTGCTGGCTCGCTACTTAAACATACAGTTTGTGTACAGTCTCGCTTTTACTCCTGGC 540
Db 488 GAGCTGCTGGCTCGCTACTTAAACATACAGTTTGTGTACAGTCTCGCTTTTACTCCTGGC 547
QY 541 TACACAATTTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTACATACCTATTTGT 600
Db 548 TACACAATTTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTACATACCTATTTGT 607
QY 601 ATGTCAAAATTAAGTATCAATGACTTTTCATGAGAGGGTAAATAATGATCTATGTG 660
Db 608 ATGTCAAAATTAAGTATCAATGACTTTTCATGAGAGGGTAAATAATGATCTATGTG 667
QY 661 CTTTATTTTACATTTTGGTTTCCAAATGCTCTGATATGAAGAAGTGGATCAGTTTACAGT 720
Db 668 CTTTATTTTACATTTTGGTTTCCAAATGCTCTGATATGAAGAAGTGGATCAGTTTACAGT 727
QY 721 GAAGTTTATGAGAGACCCACTACTCTTATTTGAGACAATGGGAAAAGCTGACATATGGCTT 780
Db 728 GAAGTTTATGAGAGACCCACTACTCTTATTTGAGACAATGGGAAAAGCTGACATATGGCTT 787
QY 781 ATGCGAACTCTGGAGTTTTCATTTTCTCATCTCCATTTTACCAACGTTGATTTTGT 840
Db 788 ATGCGAACTCTGGAGTTTTCATTTTCTCATCTCCATTTTACCAACGTTGATTTTGT 847
QY 841 GGAGGATTCACCT - GCAAACTCCCAAAACCCCTACCTAAGGAAATGGAGAGTTTGTACA 899
Db 848 GGAGGATTCACCTGGCAAACTCCCAAAACCCCTACCTAAGGAAATGGAGAGTTTGTACA 907
QY 900 GAGCTCTGGAGAAAATGGT 959
Db 908 GAGCTCTGGAGAAAATGGT 967
QY 960 AGCAGAAAGGGCAATGTAATTTGCAACAGCCCTTGCAGAGTCCCAAGAGTTTCTGTG 1019
Db 968 AGCAGAAAGGGCAATGTAATTTGCAACAGCCCTTGCAGAGTCCCAAGAGTTTCTGTG 1027
QY 1020 GAGATTTGACGGGAATAAACAGATGCTTTAGGTCTCAATACCTCGGCTGTACAAAGTGGAT 1079
Db 1028 GAGATTTGACGGGAATAAACAGATGCTTTAGGTCTCAATACCTCGGCTGTACAAAGTGGAT 1087
QY 1080 ACCCCAGATGACCTTCTAGGTGATCCAAAACAGAGCTTTTATTAACCTCATGCTGGAGC 1139
Db 1088 ACCCCAGATGACCTTCTAGGTGATCCAAAACAGAGCTTTTATTAACCTCATGCTGGAGC 1147

QY 1140 CAATGGCATCTATGAGGCAATCTACCATGGATCCCTATGTTGGGCAATTCAGTTGTTTT 1199
Db 1148 CAATGGCATCTATGAGGCAATCTACCATGGATCCCTATGTTGGGCAATTCAGTTGTTTT 1207
QY 1200 TGATCAACTGTATTAACATTTGCTCAATGAAGGCCAAGGAGCAGCTGTTAGATTGGACTT 1259
Db 1208 TGATCAACTGTATTAACATTTGCTCAATGAAGGCCAAGGAGCAGCTGTTAGATTGGACTT 1267
QY 1260 CAACACAATGTCTGAGTACAGACCTCTGATGCTGCTGAAATGCTGAAAGCAGTAAATTAATGATCCTTT 1319
Db 1268 CAACACAATGTCTGAGTACAGACCTCTGATGCTGAAATGCTGAAAGCAGTAAATTAATGATCCTTT 1327
QY 1320 ATATAAGAGATATTTATGAAATTTATCAAGATTTCAACATGATCAACAGTAAAGCCCT 1379
Db 1328 ATATAAGAGATATTTATGAAATTTATCAAGATTTCAACATGATCAACAGTAAAGCCCT 1387
QY 1380 GGATCGAGCAGTCTTCTGATTTGAATTTGTCTATGCCCAAAAGGAGCCAAACACCTTCG 1439
Db 1388 GGATCGAGCAGTCTTCTGATTTGAATTTGTCTATGCCCAAAAGGAGCCAAACACCTTCG 1447
QY 1440 AGTTGAGCCCAATGACCTCACCTGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTTCT 1499
Db 1448 AGTTGAGCCCAATGACCTCACCTGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTTCT 1507
QY 1500 GCTGCGCTGTGTGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTTTGTCTG 1559
Db 1508 GCTGCGCTGTGTGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTTTGTCTG 1567
QY 1560 GAAATTTGCTAGAAAAGGAAAGGAAAGAGATTTAGTTATGCTGACATTTGAAGC 1619
Db 1568 GAAATTTGCTAGAAAAGGAAAGGAAAGAGATTTAGTTATGCTGACATTTGAAGC 1627
QY 1620 TGAACCAACAGATAGATAGGACAACTTCAGTTTATTCAGCAAGAAAGAAAGATTTGTTA 1679
Db 1628 TGAACCAACAGATAGATAGGACAACTTCAGTTTATTCAGCAAGAAAGAAAGATTTGTTA 1687
QY 1680 TGCAGAGATTTCTTCTCTCTGTGAC 1704
Db 1688 TGCAGAGATTTCTTCTCTGTGAC 1712

RESULT 2
US-10-158-646-42
; Sequence 42, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; PRIOR FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 480489.3
US-10-158-646-42

Query Match 98.3%; Score 1693; DB 15; Length 1712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 TGCACGAGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTTAC 60
Db 8 TGCACGAGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCAGTTGTTAC 67

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QY 61 TTTAGCTCTGGAGTTGTGAAAAAGTCTGTGTGTGGCCGCGAGAAATACAGCAATTTGGATG 120
Db 68 TTTAGCTCTGGAGTTGTGAAAAAGTCTGTGTGTGGCCGCGAGAAATACAGCAATTTGGATG 127
QY 121 AATATGAAGACAATCTTGAAGAGCTTGTTCAGAGAGGTGATGAGTGCATGCTACTGGCA 180
Db 128 AATATGAAGACAATCTTGAAGAGCTTGTTCAGAGAGGTGATGAGTGCATGCTACTGGCA 187
QY 181 TCTTCAGCTTCCATCTCTTTTGTATCCCAATGATGCATCCACTCTTAATAATTGAAGTTTAT 240
Db 188 TCTTCAGCTTCCATCTCTTTTGTATCCCAATGATGCATCCACTCTTAATAATTGAAGTTTAT 247
QY 241 CCTACATCTTTAATACTAAATCTGAATTTGAGAAATATCATATGCAACAGGTTTAAGAGATGG 300
Db 248 CCTACATCTTTAATACTAAATCTGAATTTGAGAAATATCATATGCAACAGGTTTAAGAGATGG 307
QY 301 TCAGACATTCGAAAGATAGCTTTTGTATATTTTTCACAGAACCAAGAAATCCTGTGG 360
Db 308 TCAGACATTCGAAAGATAGCTTTTGTATATTTTTCACAGAACCAAGAAATCCTGTGG 367
QY 361 GAAATTATATGACATATTTAGAAACTTCTGTAAGATGTAGTTTCAAATAAGAAAGTTATG 420
Db 368 GAAATTATATGACATATTTAGAAACTTCTGTAAGATGTAGTTTCAAATAAGAAAGTTATG 427
QY 421 AAAAAAATACAGAGTCAAGATTTGACATCGTTTTTCAGATGCTGTTTTTCCCTGTGGT 480
Db 428 AAAAAAATACAGAGTCAAGATTTGACATCGTTTTTCAGATGCTGTTTTTCCCTGTGGT 487
QY 481 GAGCTGCTGGCTGGCTACTTAAACATAGCGTTTGTGTACAGTCTCCCGTTTACTCCTGGC 540
Db 488 GAGCTGCTGGCTGGCTACTTAAACATAGCGTTTGTGTACAGTCTCCCGTTTACTCCTGGC 547
QY 541 TACAACATTTGAAGACGACAGTGGAGGACTGATTTTCCCTCTCATACATACCTATTGTT 600
Db 548 TACAACATTTGAAGACGACAGTGGAGGACTGATTTTCCCTCTCATACATACCTATTGTT 607
QY 601 ATGTCAAAATTAAGTGTATCAAAATGACTTTTCATGAGAGGGTAAATAATATGATCTATGTG 660
Db 608 ATGTCAAAATTAAGTGTATCAAAATGACTTTTCATGAGAGGGTAAATAATATGATCTATGTG 667
QY 661 CTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAGTGGGATCAGTTTACAGT 720
Db 668 CTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAGTGGGATCAGTTTACAGT 727
QY 721 GAAGTTTTTGAAGACCCACTACCTTATTTGAGACAATGSGAAAGCTGACATATGCTT 780
Db 728 GAAGTTTTTGAAGACCCACTACCTTATTTGAGACAATGSGAAAGCTGACATATGCTT 787
QY 781 ATGCGAAACTCCTGGAGTTTTCATTTTCCCTCATCCATTTTACCAACGTTGATTTTGT 840
Db 788 ATGCGAAACTCCTGGAGTTTTCATTTTCCCTCATCCATTTTACCAACGTTGATTTTGT 847
QY 841 GGAGATTCCACT-GCAAACTGCAAAACCCCTACCTAAGAAATGAGAGGATTTGTACA 899
Db 848 GGAGATTCCACTGCGAAACCTGCAAAACCCCTACCTAAGAAATGAGAGGATTTGTACA 907
QY 900 GAGCTCTGGAGAAATGCTGTGTGTGTTTTCTCTGSGGTGCTGATAGTACATGAC 959
Db 908 GAGCTCTGGAGAAATGCTGTGTGTGTTTTCTCTGSGGTGCTGATAGTACATGAC 967
QY 960 AGCAGAAAGGCGCAATGTAAATTGCAACAGCCCTTGCACCAAGATCCCAAAAGGTTCTGTG 1019
Db 968 AGCAGAAAGGCGCAATGTAAATTGCAACAGCCCTTGCACCAAGATCCCAAAAGGTTCTGTG 1027
QY 1020 GAGATTTGACGGGAATAAACAGATGCTTAAAGTCTCAATCTCGGTGTACAGTGGAT 1079
Db 1028 GAGATTTGACGGGAATAAACAGATGCTTAAAGTCTCAATCTCGGTGTACAGTGGAT 1087
QY 1080 ACCCAGATACCTCTTAGGTCTACCAAAACAGAGCTTTTATACTCATGTGGGAC 1139
Db 1088 ACCCAGATACCTCTTAGGTCTACCAAAACAGAGCTTTTATACTCATGTGGGAC 1147
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QY 1140 CAATGGCATCTATGAGCAATCTACCATGGATCCCTTATGGTGGGCAATCCATTTGTTTT 1199
Db 1148 CAATGGCATCTATGAGCAATCTACCATGGATCCCTTATGGTGGGCAATCCATTTGTTTT 1207
QY 1200 TGATCAACCTGATAACATTTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGAATT 1259
Db 1208 TGATCAACCTGATAACATTTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGAATT 1267
QY 1260 CAACACAATGTCGAGTACAGACCTGCTGAATGCATGAAGACAGTAAATTAATGATCCTTT 1319
Db 1268 CAACACAATGTCGAGTACAGACCTGCTGAATGCATGAAGACAGTAAATTAATGATCCTTT 1327
QY 1320 ATATAAGAGAAATATTATGAATAATCAAGAAATCAACATGATCAACCAAGTAAAGCCCTT 1379
Db 1328 ATATAAGAGAAATATTATGAATAATCAAGAAATCAACATGATCAACCAAGTAAAGCCCTT 1387
QY 1380 GGATCCAGCAGTCTCTGGAATGCAATTTGTCATGCCCAAAAGGAGCCAAACACCTTCG 1439
Db 1388 GGATCCAGCAGTCTCTGGAATGCAATTTGTCATGCCCAAAAGGAGCCAAACACCTTCG 1447
QY 1440 AGTTGAGCCCATGACCTCACTCTGCTGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTTCT 1499
Db 1448 AGTTGAGCCCATGACCTCACTCTGCTGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTTCT 1507
QY 1500 GCTGGCTGTGTGGCAACTGTGATATTATATCATCAACAAAGTTTTGCTGTTTCTGTTCTG 1559
Db 1508 GCTGGCTGTGTGGCAACTGTGATATTATATCATCAACAAAGTTTTGCTGTTTCTGTTCTG 1567
QY 1560 GAAGTTTGTCTAGAAAAGGGAAGGAAAGGAAAGAGATTTAGTTATGCTGACATTTGAAGC 1619
Db 1568 GAAGTTTGTCTAGAAAAGGGAAGGAAAGGAAAGAGATTTAGTTATGCTGACATTTGAAGC 1627
QY 1620 TGAAAAACAGATAGATAGGACAACCTTCAGTTTATTTCCAGCAAGAAAGAAAGATTGTTA 1679
Db 1628 TGAAAAACAGATAGATAGGACAACCTTCAGTTTATTTCCAGCAAGAAAGAAAGATTGTTA 1687
QY 1680 TGCAAGATTTCTTTCTTCTCTGTGAC 1704
Db 1688 TGCAAGATTTCTTTCTTCTCTGTGAC 1712
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RESULT 3

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US-10-198-846-13134
; Sequence 13134, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13134
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2824, 2825, 2826, 2827, 2828, 2829, 2830, 2831, 2832, 2833,
; LOCATION: 2834, 2835, 2836, 2837, 2838, 2839, 2840, 2841, 2842, 2843,
; LOCATION: 2844
; OTHER INFORMATION: n = A, T, C or G
US-10-198-846-13134
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Query Match

92.0%; Score 1584.2; DB 15; Length 2844;

	Best Local Similarity	95.4%	Pred. No. 0;	Mismatches	78;	Indels	0;	Gaps	0;
	Matches	1631;	Conservative	0;					
Qy	1	TGACACAGGATGACTCTGAAATGGACATTCACTTCTGCTGTATACATCTCAGTTGTTAC	60						
Db	25	TGCACCAGGATGACTCTGAAATGGACATTCACTTCTGCTGTATACATCTCAGTTGTTAC	84						
Qy	61	TTTTAGCTCTCGGAGTTGTGGAAAGTGCTGGTGTGGCCGACAGAATAACGCCAATGGATG	120						
Db	85	TTTTAGCTCTCGGAGTTGTGGAAAGTGCTGGTGTGGCCGACAGAATAACGCCAATGGATG	144						
Qy	121	AATATGAAGACNATCCTGAAAGAGCTTTGTCAGAGAGGTATGAGGTGACTGTACTGGCA	180						
Db	145	AATATGAAGACNATCCTGAAAGAGCTTTGTCAGAGAGGTATGAGGTGACTGTACTGGCA	204						
Qy	181	TCCTCAGCTCCCATTCCTTTTGTATCCCAATGATGCATCCCACTCTTAATAATTGAAGTTTAT	240						
Db	205	TCCTCAGCTCCCATTCCTTTTGTATCCCAATGATGCATCCCACTCTTAATAATTGAAGTTTAT	264						
Qy	241	CCTACATCTTTAACTAAAACGTAATTTGAGAATATCATATGCAACAGGTTAAAGATGG	300						
Db	265	CCTACATCTTTAACTAAAACGTAATTTGAGAATATCATATGCAACAGGTTAAAGATGG	324						
Qy	301	TCAGACATTCGAAAAAGATAGCTTTTGGTTATATTTTTCACAAGNAACGAAGAAATCCTGTGG	360						
Db	325	TCAGACATTCGAAAAAGATAGCTTTTGGTTATATTTTTCACAAGNAACGAAGAAATCCTGTGG	384						
Qy	361	GAATTAATGACATATTTAGAAACCTCTGTAAAGATGTAGTTTCAAATAAGAAGTTTATG	420						
Db	385	GAATTAATGACATATTTAGAAACCTCTGTAAAGATGTAGTTTCAAATAAGAAGTTTATG	444						
Qy	421	AAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTCCCTGTGGT	480						
Db	445	AAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTCCCTGTGGT	504						
Qy	481	GAGCTGCTGGTGGCTACTTTAAACATACGGTTTGTGTACAGTCTCCCGTTTATCTCTGGC	540						
Db	505	GAGCTGCTGGTGGCTACTTTAAACATACGGTTTGTGTACAGTCTCCCGTTTATCTCTGGC	564						
Qy	541	TACACAATTTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTCACATACCTATTTGTT	600						
Db	565	TACACAATTTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTCACATACCTATTTGTT	624						
Qy	601	ATGTCAAAATTTAAGTGTACAAATGACATTTTCATGGAGAGGGTAAAAAATATGATCTATGTG	660						
Db	625	ATGTCAAAATTTAAGTGTACAAATGACATTTTCATGGAGAGGGTAAAAAATATGATCTATGTG	684						
Qy	661	CTTTATTTTGTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAGT	720						
Db	685	CTTTATTTTGTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAGT	744						
Qy	721	GAGTTTTTAGAGAGACCCACTACCTTATTTGAGACATGGAAGCTGACATATGGCTT	780						
Db	745	GAGTTTTTAGAGAGACCCACTACCTTATTTGAGACATGGAAGCTGACATATGGCTT	804						
Qy	781	ATGCGAAATCTCTGGAGTTTTCAAATTTCCCTCATCCATTTCTTACCAAACGTTGATTTGTT	840						
Db	805	ATGCGAAATCTCTGGAGTTTTCAAATTTCCCTCATCCATTTCTTACCAAACGTTGATTTGTT	864						
Qy	841	GGAGGATTCACATGCAAAACCTGCGAAAACCCCTACCTTAAGGAAATGGAGGAGTTGTACAG	900						
Db	865	GGAGGATTCACATGCAAAACCTGCGAAAACCCCTACCTTAAGGAAATGGAGGAGTTGTACAG	924						
Qy	901	AGCTCTGGAGAAATAGTGTGTGGTGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGACA	960						
Db	925	AGCTCTGGAGAAATAGTGTGTGGTGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGACA	984						
Qy	961	GCAGAAAGGGCCAATGTAATTGCAACAGCCCTTCGCCAAGATCCCACAAAAGGTTCTGTGG	1020						
Db	985	GCAGAAAGGGCCAATGTAATTGCAACAGCCCTTCGCCAAGATCCCACAAAAGGTTCTGTGG	1044						
Qy	1021	AGATTTTCAACGGGAATAAACACAGATGCTTATAGTCTCAATACTCGGCTGTACAAATGGAATA	1080						

Qy	1021	AGATTTGACGGGAATAAACCAGATGCTTAGTGTCTCAATACTCGGCTGTACAAGTGGATA	1081
Db	1026	AGATTTGATGGGAATAAACCCAGATACCTTAGTGTCTCAATACTCGGCTGTATAAGTGGATA	1085
Qy	1081	CCCAGAAATCACCTTCTAGTGTATCCAAAAACACAGAGCTTTTATATACTCATGCTGGAGCC	1140
Db	1086	CCCAGAAATCACCTTCTAGTGTATCCAAAGACAGAGCTTTTATACTCATGCTGGAGCC	1145
Qy	1141	AATGGCATCTATCAGGCAATCTACCATGGGATCCCTATGCTGGGCAATCCATTTGTTTTT	1200
Db	1146	AATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGCTGGGGAATCCATTTGTTGCC	1205
Qy	1201	GATCAACCTGATAAACATTTGCTACATGAAGGCCCAAGGAGCAGCTGTTAGATTTGGACTTC	1260
Db	1206	GATCAACCTGATAAACATTTGCTACATGAAGGCCCAAGGAGCAGCTGTTAGATTTGGACTTC	1265
Qy	1261	AACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCCTTA	1320
Db	1266	AACACAATGTCGAGTACAGACTTGTCTGAATGCAATTTGAAGAGAGTAATTAATGATCCCTTA	1325
Qy	1321	TATAAAGAGAAATATTATGAAATTTATCAAGAAATTCACACATGATCAACACAGTAAAGCCCTCG	1380
Db	1326	TATAAAGAGAAATCTTATGAAATTTATCAAGAAATTCACATGATCAACACAGTAAAGCCCTCG	1385
Qy	1381	GATCGAGCAGCTTCTCGGAATTTGATGTAATTTGTCATGCCCAACAAAGAGCCAAACACCTTCGA	1440
Db	1386	GATCGAGCAGCTTCTCGGAATTTGATGTAATTTGTCATGCCCAACAAAGAGCTAAACACCTTCGG	1445
Qy	1441	GTTCGAGCCCATGACCTCACCTGGTTCCAGTACCACCTCTTTGGATGATGATGGTTCTCG	1500
Db	1446	GTTCGAGCCCATGACCTCACCTGGTTCCAGTACCACCTCTTTGGATGATGATGGTTCTCGCTG	1505
Qy	1501	CTGGCTGTGTGCGCAACTGTGATATTATCATCAAAAGTTTTGTCTGTCTTTCTTTCTCTGG	1560
Db	1506	CTGGCTGTGTGCGCAACTGTGATATTATCGTCACAAAATGTTGTCTGTCTTTCTTTCTCTGG	1565
Qy	1561	AGTTTGTCTAGAAAAGGGGAAGAGGAAAAGAGATTAGTTATGCTGCACATTTGAAGCT	1620
Db	1566	AGTTTGTCTAGAAAAGCAAGAGGGAAGAAAATGATTAGTTATCTGAGATTTGAAGCT	1625
Qy	1621	GGAAAACCATAGATAGGACAACTTCAGTTTATTCAGCAAGAAAAGAAAGATTGTTAT	1680
Db	1626	GGAAAACCATGATAGGTGAGACTACTTCAGTTTATTCAGCAAG-----AAAGATTCTGAT	1680
Qy	1681	GCAAGATTTCTTTCTTCTCTGTGACAAAAAAGAAAAAAGAAAAA 1722	
Db	1681	GCAAGATTTCTTTCTTCTCTGAGCAAAAAAAGAAAAAAGAAAAA 1722	
RESULT 5			
US-09-968-007A-368			
; Sequence 368, Application US/09968007A			
; Publication No. US20040115625A1			
; GENERAL INFORMATION:			
; APPLICANT: Ebner, Reinhard			
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using			
; TITLE OF INVENTION: Gene Sets			
; FILE REFERENCE: 689290-71			
; CURRENT APPLICATION NUMBER: US/09/968, 007A			
; CURRENT FILING DATE: 2001-10-02			
; PRIOR APPLICATION NUMBER: US/60/237,172			
; PRIOR FILING DATE: 2000-10-02			
; PRIOR APPLICATION NUMBER: US/60/237,173			
; PRIOR FILING DATE: 2000-10-02			
; PRIOR APPLICATION NUMBER: US/60/237,278			
; PRIOR FILING DATE: 2000-10-02			
; PRIOR APPLICATION NUMBER: US/60/237,294			
; PRIOR FILING DATE: 2000-10-02			
; PRIOR APPLICATION NUMBER: US/60/237,295			
; PRIOR FILING DATE: 2000-10-02			
; PRIOR APPLICATION NUMBER: US/60/237,316			
; PRIOR FILING DATE: 2000-10-02			
; NUMBER OF SEQ ID NOS: 1,001			

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 168
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-368

Query Match 86.0%; Score 1481.2; DB 11; Length 1855;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 138; Indels 5; Gaps 1;

QY 1 TGCACGAGTACTCTGAAATGCACTTCAGTTCCTCTGCTGATACATCTCAGTTCGTAC 60
DB |||||
6 TGCACGAGATGCTGTGAAATGCACTTCAGTTCCTCTGCTGATACATCTCAGTTCGTAC 65
QY 61 TTTAGCTCTGGGAGTTGTGGAAAAGTGTGGTGTGGGCCCGCAAGATACAGCCATTGGATG 120
DB |||||
66 TTTAGCTCTGGGAAATGTGGAAAAGTGTGGTGTGGGCCAGCAGATACAGCCATTGGATG 125
QY 121 AATATGAAGACATCTGAAAGAGCTTGTTCAGAGAGTTCATGAGTGTACTGTGGCA 180
DB |||||
126 AATATAAAGACAACTCTGATGAGCTTATTTCAAGAGAGTTCATGAGTGTACTGTGGCA 185
QY 181 TCTTCAGCTTCCATCTCTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAATTTAT 240
DB |||||
186 TCTTCAGCTTCCATCTCTTTGATCCCAACTCATCCGCTTAAATTTGAAATTTAT 245
QY 241 CTTACATCTTTAACTAAACTGAAATTTGAGAAATATCATCATGCAACAGCTTAAGAGATGG 300
DB |||||
246 CCCACATCTTTAACTAAACTGAAATTTGAGAAATTTTTCATCATGCAACAGATTAAGAGATGG 305
QY 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAGAACAGAAATCTCTGG 360
DB |||||
306 TCAGACCTTCCAAAGATACATTTTGGTTATATTTTTCACAAAGTACAGGAAATCATGTCA 365
QY 361 GAAATTTATGACATATTTAGAAATCTCTGTAAGATGTAGTTTCAATTAAGAAAGTTATG 420
DB |||||
366 ATATTTGGTGACATACTAGAAAGTCTGTAAAGATGTAGTTTCAATTAAGAAATTTATG 425
QY 421 AAAAACTACAGAGTCAAGATTTGACATCGTTTTCAGAGATGCTGTTTTCCCTGTGT 480
DB |||||
426 AAAAAAGTACAGAGTCAAGATTTGACATCGTTTTCAGAGATGCTATTTTTCCCTGTAGT 485
QY 481 GAGCTCTGCTGCTGCTACTTAACTACATCGTTTGTGTCAGTCTCCGCTTACTCTCTGGC 540
DB |||||
486 GAGCTCTGCTGCTGCTATTTACATACCTTTGTGTACAGTCTCAGCTTCTCTCTGGC 545
QY 541 TACACAATTTGAAAGGCACAGTGGAGGACTGATTTTCCCTCTCTTCTACATACCTATTGTT 600
DB |||||
546 TACACTTTTGAAGACATAGTGGAGGATTTATTTTCCCTCTCTTCTACCTACCTGTTGTT 605
QY 601 ATGTCAAAATTAAGTGATCAAAATGACTTTTCATGGAGAGGGTAAAAATATGATCTATG 660
DB |||||
606 ATGTCAAGAAATTAAGTGATCAAAATGACTTTTCATGGAGAGGGTAAAAATATGATCTATG 665
QY 661 CTTTATTTTGGCTTTTGGTTCCAAATGTCTGATATGAAGAGTGGGATCAGTTTTACAGT 720
DB |||||
666 CTTTATTTTGGCTTTTGGTTCCAAATGTCTGATATGAAGAGTGGGATCAGTTTTATAGT 725
QY 721 GAAGTTTGAAGAGCCCACTACTCTTATTTGAGACAAATGGGAAAGCTGACATATGGCTT 780
DB |||||
726 GAAGTTTGAAGAGCCCACTACTCTTATCTGAGACAAATGGGAAAGCTGACATATGGCTT 785
QY 781 ATGCGAAATCTCTGGAGTTTCAATTTCTCATCCATTTCTTACCAACGCTGATTTGTT 840
DB |||||
786 ATTCGAAATCTCTGGAAATTTTTCAGTTTCTCTCATCCACTCTTACCAAAATTTGATTTGTT 845
QY 841 GGAGGATTCACATGCAAACTGCAAAACCTTACCTTAAAGGAAATGGAGGAGTTGTACAG 900
DB |||||
846 GGAGGATTCACATGCAAACTGCAAAACCTTACCTTAAAGGAAATGGAGGAGTTGTACAG 905
QY 901 AGCTCTGGAGAAATAGGTGTGTGGTGTGTTTCTCTGGGGTCAAGTAAAGTAAACATGACA 960
DB |||||

DB 906 AGCTCTGGAGAAAATGGTGTGTGTGTTTCTCTGGGGTCAATGGTCAATGATGACA 965
QY 961 GCAGAAAGGGCCAAATGTATTTGCAACAGCCCTTGCACAGATCCCAACAAAGTTCTGTGG 1020
DB |||||
966 GAAAGAAAGGGCCAAAGTATTTGCAATCAGCCCTGGCCAGATCCCAACAAAGTTCTGTGG 1025
QY 1021 AGATTTGACGGGAATAAAACAGATGCCCTTAGTCTCAATACTCGGCTGTACAAGTGGATA 1080
DB |||||
1026 AGATTTGATGGGAATAAAACAGATACCTTAGGTCTCAATACTCGGCTGTATAAGTGGATA 1085
QY 1081 CCCAGAAATGACCTTCTAGGTTCATCAAAACAGAGCTTTTATAACTCATGCTGGAGCC 1140
DB |||||
1086 CCCAGAAATGACCTTCTAGGTTCATCAAAAGACAGAGCTTTTATAACTCATGCTGGAGCC 1145
QY 1141 AATGCATCTATGAGGCAATCTACCATGGATCCCTATGTTGGGCAATTCATGTTTTTTT 1200
DB |||||
1146 AATGCATCTACGAGCAATCTACCATGGATCCCTATGTTGGGCAATTCATGTTTTTTT 1205
QY 1201 GATCAACCTGATACATTTGCTCAATGAAGCCCAAGGAGCAGCTGTAGATTGGACTTC 1260
DB |||||
1206 GATCAACCTGATACATTTGCTCAATGAAGCCCAAGGAGCAGCTGTAGATTGGACTTC 1265
QY 1261 AACCAATGTCCAGTACAGACCTGCTGAATGCATGAAGACAGTAAATTAATGATCTTTA 1320
DB |||||
1266 AACCAATGTCCAGTACAGACTTGTGATGCAATGAAGAGAGTAAATTAATGATCTTTA 1325
QY 1321 TATAAGAGAAATATTAATGAATTAATCAAGAAATTAACATGATCAACAGTAAAGCCCTG 1380
DB |||||
1326 TATAAGAGAAATGTTATGAATTAATCAAGAAATTAACATGATCAACAGTAAAGCCCTG 1385
QY 1381 GATCCAGCAGTCTCTGGATTAATTTGTGATGCAATTTGTCATGCCCAAGAGGAGCTT 1440
DB |||||
1386 GATCCAGCAGTCTCTGGATTAATTTGTGATGCAATTTGTCATGCCCAAGAGGAGCTT 1445
QY 1441 GTTCAGGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTTGGTTCTG 1500
DB |||||
1446 GTTCAGGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTTGGTTCTG 1505
QY 1501 CTGGCTGTGTGGCAATCTGTGATATTTATCATCAAAAGTTTGTCTGTTTGTCTGTGG 1560
DB |||||
1506 CTGGCTGTGTGGCAATCTGTGATATTTATCGTCACAAAATGTTGTCTGTTTGTCTGTGG 1565
QY 1561 AAGTTTGTAGAAAAGGGAAGGAAAGAGATTAAGTATGCTGACATTTTGAAGCT 1620
DB |||||
1566 AAGTTTGTAGAAAAGGGAAGGAAAGAGATTAAGTATGCTGACATTTTGAAGCT 1625
QY 1621 GGAACACAGATAGATAGCAACTTCAGTTTATTTCCAGCAAGAAAAGAAATTTGTTAT 1680
DB |||||
1626 GGAACACCTGATAGTGTAGACTTCTCAGTTTATTTCCAGCAAG----AAAGATTGTGAT 1680
QY 1681 GCAAGATTTCTTCT 1722
DB 1681 GCAAGATTTCTTCT 1722

RESULT 6

US-09-968-007A-735
; Sequence 735, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signal
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294

; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-783-528-57

Query Match 86.0%; Score 1481.2; DB 21; Length 1855;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 138; Indels 5; Gaps 1;

QY 1 TGCACAGGATGACTGTAATGGACTTCAGTCTCTCTGCTGATACATCTCAGTGTCTTAC 60
Db TGCACAGGATGCTGTGAATGGACTTCAGTAAATTTTGTCTAATACTAGACTTTTGC 65

QY 61 TTTAGCTCTGGGAGTTGTGGAAAAGTGTGGTGGGCGCGAGAAATACAGCCATTGGATG 120
Db TTTAGCTCTGGGAATTTGTGAAAAGTGTGGTGGGCGAGCAATACAGCCATTGGATG 125

QY 121 AATATGAAGACAATCTGAAAAGCTTTGTTCAGAGAGTCTAGAGTGACTGTACTGGCA 180
Db AATATAAAGACAACTCTGATGAGCTTATTTCAGAGAGGTCTAGAGTGACTGTACTGGCA 185

QY 181 TCTTCAGCTTCCATCTCTTTTTCATCCCAATGATGATCCACTCTTAAATTTCAAGCTTAT 240
Db TCTTCAGCTTCCATCTCTTTTTCATCCCAACTCACTCATCCGCTCTTAAATTTGAAATTTAT 245

QY 241 CCTACATCTTTAACTAAAACACTGAAATTTGAGAATATCATCATGCAACAGAGTTAAGATGG 300
Db CCCACATCTTTAACTAAAACACTGAGTTGGAGATTTTCATCATGCAACAGATTAAGATGG 305

QY 301 TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCAGAGAAACAAGAAATCCTGTGG 360
Db TCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCAGAGTACAGGAAATCATGTCA 365

QY 361 GAATATATGACATATTTAGAACTCTCTGAAGATGTAGTTTCAATAAGAAAGTTATG 420
Db ATATTGGTGACATACATAGAAAGTCTCTGAAGATGTAGTTTCAATAAGAAATTTATG 425

QY 421 AAAAACTACAAGAGTCAAGATTTGACATCGTTTTTTCAGAGATGCTGTTTTTCCCTGTGTG 480
Db AAAAAAGTACAAGAGTCAAGATTTGACGTCAATTTTTCAGAGATGCTATTTTCCCTGTACT 485

QY 481 GAGCTGCTGGCTCGCTACTTTAACATACCGTTTGTGTACAGTCTCGCTGTACTCTCTGGC 540
Db GAGCTGCTGGCTGAGCTATTTAACATACCCCTTTTGTGTACAGTCTCAGCTTCTCTCTGGC 545

QY 541 TACACAAATTTGAAGGCACAGTGGAGACTGATTTTCCCTCTTCTTACATACCTATTGTT 600
Db TACACTTTTGAAGAGCATAGTGGAGATTTATTTTCCCTCTTCTTACATACCTATTGTT 605

QY 601 ATGTCAAAATTAAGTGATCAAAATGACTTTTCATGGAGAGGTAAAAATATGATCTATGTG 660
Db ATGTCAAGAAATTAAGTGATCAAAATGACTTTTCATGGAGAGGTAAAAATATGATCTATGTG 665

QY 661 CTTTATTTTGACTTTTGGTTTCAAATGTCTGATATGAAGAGTGGATCAGTTTTTACAGT 720
Db CTTTACTTTTGACTTTTGGTTTCAAATATTTTGATCATGAAGAGTGGATCAGTTTTTATAGT 725

QY 721 GAAGTTTTAGGAAGACCCACTACCTTATTTTGAGACAAATGGGAAAAGCTGACATATGGCTT 780
Db GAAGTTCTAGGAAGACCCACTACCTAGTTATCTGAGACAAATGGGAAAAGCTGACGATGGCTT 785

QY 781 ATCGAAACTCTCGAGTTTTCAAATTTCTCTCATCTCAATTTCTTACCAAACTGTGATTTGTT 840
Db ATTCGAAACTCTCGAAATTTTTCAGTTTCTCTCATCTCACTTCTTACCAAACTGTGATTTGTT 845

QY 841 GGAGAGTCCATCTGCAAACTGCGAAACCCCTACCTTAAGGAAATGGAGAGTTTGTACAG 900
Db GGAGAGCTCACTGCAAACTGCGAAACCCCTGCTTAAGGAAATGGAGAGTTTGTACAG 905

QY 901 AGCTCTGGAGAAAATGGTGTGGTGTGTTTTCTCTGGGCTCAGTATAGTAACATGACA 960
Db AGCTCTGGAGAAAATGGTGTGGTGTGTTTTCTCTGGGCTCAATGGTCAATAGTAACATGACA 965

QY 961 GCAGAAAAGGCCCAATGTAAATTCGCAACAGCCCTTGCACAGATCCCAAAAAGTTCTGTGG 1020
Db GAAAGAAAGGCCCAAGTAAATTCGATCAGCCCTGGCCAGATCCCAAAAAGTTCTGTGG 1025

QY 1021 AGATTTGACGGGAATAAACCAGATGCTTAGTGTCTCAATPACTCGGCTGTACAGTGGATA 1080
Db AGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATPACTCGGCTGTATAAGTGGATA 1085

QY 1081 CCCAGAAATGACTTCTAGTGTATCCAAAACAGAGCTTTTATAACTCATCGTGAGGCC 1140
Db CCCAGAAATGACTTCTAGTGTATCCAAAACAGAGCTTTTATAACTCATCGTGAGGCC 1145

QY 1141 AATGCAATCTATGAGGCAATCTACCATGGGATCCCTATGTTGGGCAATTCATTTGTTTTT 1200
Db AATGCAATCTACGAGCAATCTACCATGGGATCCCTATGTTGGGATTCATTTGTTGCC 1205

QY 1201 GATCAACCTGATAAATGCTCACAATGAAGGCCAAGGGAGCAGCTGTTHAGATTGCACTTC 1260
Db GATCAACCTGATAAATGCTCACAATGAAGGCCAAGGGAGCAGCTGTTHAGATTGCACTTC 1265

QY 1261 AACCAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCCTTA 1320
Db AACCAATGTCGAGTACAGACTTGTCTGAATGCAATGCAAGAGAGTAATTAATGATCCCTTA 1325

QY 1321 TATAAGAGAATATTTATGAAATTTCAAGAATTTCAACATGATCAACCCAGTAAAGCCCTTG 1380
Db TATAAGAGAATGTTATGAAATTTATCAAGAATTTCAACATGATCAACCCAGTAAAGCCCTTG 1385

QY 1381 GATCAGCAGTCTTCTCGGATGAAATTTGTTCATGCCCAAGAGGCGCAAAACACCTTCA 1440
Db GATCAGCAGTCTTCTCGGATTTGAATTTGTTCATGCCCAAGAGGAGCTAAACACCTTCCG 1445

QY 1441 GTTGAGCCCATGACCTCACCTGGTTCCAGTACCCTCTTTTCGATGTGATGGGTTCTG 1500
Db GTTGAGCCCATGACCTCACCTGGTTCCAGTACCCTCTTTTCGATGTGATGGGTTCTG 1505

QY 1501 CTGGCTGTGTGGCAACTGTGATATTTATCATCACAAGTTTGTCTGTTTTGTTTCTGG 1560
Db CTGGCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGTTCTGG 1565

QY 1561 AGTTTGTCTAGAAAAGGGAAGAGGAAAAGAGATTAGTTATGCTGCAATTTGAGCT 1620
Db AGTTTGTCTAGAAAAGGGAAGGAAAAGAGAAAATGATTAGTTATGCTGAGATTTGAGCT 1625

QY 1621 GGAAAAACAGATAGATAGCAAACTTCAGTTTATTTCCAGCAAGAAAAGATTGTTAT 1680
Db GGAAAAACCTGATAGGTGAGACTTCTCAGTTTATTTCCAGCAAG-----AAAGATTGTGAT 1680

QY 1681 GCAAGATTTCTTTCTCTCTGTGACAAAAAATAAAAAA 1722
Db GCAAGATTTCTTTCTCTCTGACAAAAAATAAAAAA 1722

RESULT 8

US-10-843-641A-6838
; Sequence 6838, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: Signature Gene Sets
; CURRENT FILING DATE: 2004-05-12
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456

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; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6838
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1855)
; OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-6838

Query Match      86.08; Score 1481.2; DB 22; Length 1855;
Best Local Similarity 91.74; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 138; Indels 5; Gaps 1;

QY      1  TGCACAGGATGACTCTGAAATGACCTTCAGTTCTCTGCTGATACATCTCAGTTGTTC 60
DB      6  TGCACAGGATGCTGTGAAATGGACTTCAGTAATTTGCTAATACAACTGACCTTTGC 65

QY     61  TTTAGCTCTGGAGTTGTGGAAGTCTGGTGTGGGCCGACAGAAATACAGCCATTGGATG 120
DB     66  TTTAGCTCTGGGAATTTGTGGAAGTCTGGTGTGGGCAGCAGAAATACAGCCATTGGATG 125

QY    121  AATATGAAGACAATCTGGAAGAGCTGTTTTCAGAGAGTCTGATGAGTCTGAGTCTGACGCA 180
DB    126  AATATAAGACAATCTGGAAGAGCTGTTTTCAGAGAGTCTGATGAGTCTGAGTCTGACGCA 185

QY    181  TCTTCAGCTTCCATCTCTTTTGTATCCCAATGATGCACTCCACTCTTAAATTTGAAGTTTAT 240
DB    186  TCTTCAGCTTCCATCTCTTTTGTATCCCAACAACTCATCCGCTCTTAAATTTGAATTTAT 245

QY    241  CCTACATCTTTAACTAAACTGAAATTTGAGAATATCATCATGCAACAGGTAAAGATGG 300
DB    246  CCCACATCTTTAACTAAACTGAGTTGGAGAAATTTTCATCATGCAACAGATTAAGAGATGG 305

QY    301  TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCACAGAAACAAGAAATCCCTGTGG 360
DB    306  TCAGACCTTCCAAAGATACATTTTGGTTATATTTTTCACAGTACAGGAAATCATGTCA 365

QY    361  GAATTTATATGACATATTTAGAAACTCTCTGTAAGAGATGAGTTTCAAATAGAAAGTTATG 420
DB    366  ATATTTGGTGACATATGACATAGAAAGTCTGTAAGAGATGAGTTTCAAATAGAAATTTATG 425

QY    421  AAAAACTACAAGAGTCAAGATTGACATCGTTTTTTCAGAGATGCTGTTTTCCCTCTGGT 480
DB    426  AAAAAAGTACAAGAGTCAAGATTGACATCGTTTTTTCAGAGATGCTGTTTTCCCTCTGGT 485

QY    481  GAGCTGCTGCTGCTGCTGCTTACATAGGTTTGTGTACATGCTCCGCTTACCTCTGGC 540
DB    486  GAGCTGCTGCTGCTGCTGCTTACATAGGTTTGTGTACATGCTCTCAGCTTCTCTCTGGC 545

QY    541  TACACAAATGAAAGGACAGTGGAGGACTGATTTTCCCTCTCTACATACCTATTGTT 600
DB    546  TACACATTTGAAAGGACATAGTGGAGGATTTATTTCCCTCTCTCTACCTAGCTGTTGT 605

QY    601  ATGTCAAAATTAAGTATCAAAATGACCTTTCATGGAGGGGTAAATAATATGATCTATGTG 660
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DB    606  ATGTCAGAAATTAACATGATCAAAATGACTTTCATGGAGAGGGTAAATAATATGATCTATGTG 665
QY    661  CTTTATTTTACATCTTTGGTTCCAAATGCTCTGATATGAAGAGTGGGATCAGTTTACAGT 720
DB    666  CTTTATCTTTGACTTTTGGTTTCGAAATATTTGATGATGAAGAGTGGGATCAGTTTATAGT 725
QY    721  GAAATTTTATAGGAAGAGCCCACTACCTTATTTGAGACAATGGGAAAGCTGACATATGGCTT 780
DB    726  GAAATTTCTAGGAAGAGCCCACTACCTTATCTGAGACAATGGGAAAGCTGACATATGGCTT 785
QY    781  ATCGGAAATCTCTGGAGTTTTCATTTCTCTCATCTCATCTTACCAAACGTTGATTTGTT 840
DB    786  ATTTCGAAATCTCTGGAAATTTTTCAGTTTCTCTCATCTCATCTTACCAAATGTTGATTTGTT 845
QY    841  GGAGGATTCACATGCAAAACCTGCAAAACCTCTACCTAAGGAAATGGAGGAGTTGTACAG 900
DB    846  GGAGGATTCACATGCAAAACCTGCAAAACCTGCAAAACCTGCTAAGGAAATGGAGGAGTTGTACAG 905
QY    901  AGCTCTGGAGAAATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
DB    906  AGCTCTGGAGAAATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 965
QY    961  GCAGAAAGGCCCAATGTAATTTGCAACAGCCCTTGGCCAAAGATCCCAAAAGGTTCTGTGG 1020
DB    966  GAAGAAAGGCCCAACGTAATTTGCAATCAGCCCTGGCCCAAGATCCCAAAAGGTTCTGTGG 1025
QY   1021  AGATTTTGACGGGAATAAACCAGATGCTTGTAGTCTCAATACTCGGCTGTACAGTGCATAT 1080
DB   1026  AGATTTTGAGGGGAATAAACCAGATGCTTGTAGTCTCAATACTCGGCTGTATAGTGCATAT 1085
QY   1081  CCCAGAAATGACCTTCTAGGTCTATCCAAAAACAGAGCTTTTATTAACATCATGTGGAGCC 1140
DB   1086  CCCAGAAATGACCTTCTAGGTCTATCCAAAGACAGAGCTTTTATTAACATCATGTGGAGCC 1145
QY   1141  AATGGCATCTATGAGGCAATCTAATGAGGATCCCTATGTTGGGATTCCTCATTTGTTTTT 1200
DB   1146  AATGGCATCTATGAGGCAATCTAATGAGGATCCCTATGTTGGGATTCCTCATTTGTTTTT 1205
QY   1201  GATCAACCTGATAAATGCTCAATGAGGCAAGGCAAGGAGGAGCAGCTGTAGATGGACTTC 1260
DB   1206  GATCAACCTGATAAATGCTCAATGAGGCAAGGCAAGGAGGAGCAGCTGTAGATGGACTTC 1265
QY   1261  AACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAAATTAATGATCTCTTA 1320
DB   1266  AACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAAATTAATGATCTCTTA 1325
QY   1321  TATAAAGAGAAATATTAATGAATTTATCAAGAAATTTCAACATGATCAACAGTAAAGCCCTG 1380
DB   1326  TATAAAGAGAAATGTTATGAATTTATCAAGAAATTTCAACATGATCAACAGTAAAGCCCTG 1385
QY   1381  GATCGAGAGAGTCTTCTGGATTTGAATTTGTCATGCCCAAGAGGAGGCAACACCTTCGA 1440
DB   1386  GATCGAGAGAGTCTTCTGGATTTGAATTTGTCATGCCCAAGAGGAGGCAACACCTTCGG 1445
QY   1441  GTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATGGTGTCTG 1500
DB   1446  GTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATGGTGTCTG 1505
QY   1501  CTGGCTGTGTGGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTGTTTGTCTGTG 1560
DB   1506  CTGGCTGTGTGGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTGTTTGTCTGTG 1565
QY   1561  AAGTTTGTCTAGAAAGGAGGAAAGGAAAGAGATTAGTTATGCTGTGACATTTGAAGCT 1620
DB   1566  AAGTTTGTCTAGAAAGGAGGAAAGGAAAGAGATTAGTTATGATGATTTGATGATTTGAAGCT 1625
QY   1621  GGAAGAACCATAGATAGGACAACTTCAGTTTATTCAGCAAGAAAGAAAGATGTTAT 1680
DB   1626  GGAAGAACCATGATAGTGAAGTACTTTCAGTTTATTCAGCAAG- - - - -AAGATTTGAT 1680
QY   1681  GCAAGATTTCTTCTCTGTGTGACAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1722
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Db 1681 GCAAGATTCTCTTCCTGACACAAAAAAGAAAAAAGAAA 1722

RESULT 9

US-10-843-641A-7205 : Sequence 7205, Application US/10843641A
: Publication No. US20050064454A1
: GENERAL INFORMATION:
: APPLICANT: Avalon Pharmaceuticals, Inc.
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
: APPLICANT: Signature Gene Sets
: FILE REFERENCE: 689290-189
: CURRENT APPLICATION NUMBER: US/10/843,641A
: CURRENT FILING DATE: 2004-05-12
: PRIOR APPLICATION NUMBER: US/09/873,367
: PRIOR FILING DATE: 2001-06-05
: PRIOR APPLICATION NUMBER: US/09/954,531
: PRIOR FILING DATE: 2001-09-18
: PRIOR APPLICATION NUMBER: US/09/954,456
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US/09/962,436
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US/09/962,832
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US/09/964,824
: PRIOR FILING DATE: 2001-09-27
: PRIOR APPLICATION NUMBER: US/09/967,768
: PRIOR FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US/09/968,007
: PRIOR FILING DATE: 2001-10-02
: PRIOR APPLICATION NUMBER: US/09/969,347
: PRIOR FILING DATE: 2001-10-02
: PRIOR APPLICATION NUMBER: US/09/969,708
: PRIOR FILING DATE: 2001-10-03
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 8447
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 7205
: LENGTH: 1855
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1855)
: OTHER INFORMATION: n=a,t,g or c

US-10-843-641A-7205

Query Match 86.0%; Score 1481.2; DB 22; Length 1855;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 138; Indels 5; Gaps 1;

Qy 1 TGCACGAGATGACTCTGAAATGGACTTCAGTCTCTCTGCTGATACATCTCAGTTGTATC 60
Db |||||
6 TGCACGAGATGCTGTGAAATGGACTTCAGTAAATTTTGCTAATACAACTGAGCTTTGC 65
|||
Qy 61 TTTAGCTCTGGGAGTTGTGGAAGTGTGGTGTGGGCGCGAGAAATACAGCCATTGGATG 120
Db |||||
66 TTTAGCTCTGGGAAATGTGGAAGGTGTGGTGTGGGCGAGAGAAATACAGCCATTGGATG 125
|||
Qy 121 AATATGAAGACAACTCTGAAAGAGCTTGTTCAGAGAGGTTCATGAGTGTACTGTGCA 180
Db |||||
126 AATATAAGACAACTCTGATGAGCTTTATTCAGAGGTTCATGAGTGTACTGTGCA 185
|||
Qy 181 TCTTCAGCTTCCATCTTTTGTATCCCAATGATGCATCCACTCTTAAATTTTGAAGTTTAT 240
Db |||||
186 TCTTCAGCTTCCATCTTTTGTATCCCAACTCATCGCTCTTTAAATTTGAAATTTAT 245
|||
Qy 241 CCTACATCTTTAACTAAACTGAAATTTGGAATATCATCATGCAACAGGTTTAAGAGATGG 300
Db |||||
246 CCACATCTTTAACTAAACTGAGTTGGAGAAATTTTCATCATGCAACAGATTAAGAGATGG 305
|||
Qy 301 TCAGACATTCGAAAGATAGCTTTTGGTTATATTTTTCAGAGAAACAGAAATTCCTCTGG 360
|||

QY 1441 GTTGACGCCCATGACCTCACTGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTCTTG 1500
DB 1446 GTTGACGCCCATGACCTCACTGTTCCAGTACCACCTCTTTGGATGTGATTTGGTTCTTG 1505
QY 1501 CTGGCTGTGTGGCACTGTGATTTATCATCAAAAGTTTGTCTGTGTTTGTCTGTG 1560
DB 1506 CTGTCTGTGTGGCACTGTGATTTATCGTCACAAAATGTCTGTGTTTGTCTGTG 1565
QY 1561 AAGTTTCTAGAAAAGGGAAGGGAAGAGATTAGTTATGTCTGTGACATTTGAAGCT 1620
DB 1566 AAGTTTCTAGAAAAGGGAAGGGAAGAGATTAGTTATGTCTGTGACATTTGAAGCT 1625
QY 1621 GGAACCAGATAGATAGGCAACTTCAGTTTATTCAGCAAGAAAAGAAAGATTGTTAT 1680
DB 1626 GGAACCCTGTAGGTGAGACTACTTCAGTTTATTCAGCAAG- - - - -AAGATTGTGAT 1680
QY 1681 GCAAGATTTCTTCTCTGTGACAAAAA - - - - - 1722
DB 1681 GCAAGATTTCTTCTCTGTGACAAAAA - - - - - 1722

RESULT 10
US-10-057-834A-1
; Sequence 1, Application US/10057834A
; Publication No. US2003009960A1
; GENERAL INFORMATION:
; APPLICANT: RATAIN, MARK J.
; APPLICANT: INNOCENTI, FEDERICO
; APPLICANT: DAS, SOMA
; APPLICANT: IYER, LALITHA
; APPLICANT: SAWYER, MICHAEL
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OPTIMIZING UGT2B7 SUBSTRATE DOSINGS
; FILE REFERENCE: ARCD-358US
; CURRENT APPLICATION NUMBER: US/10/057,834A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1991
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(1740)
US-10-057-834A-1

Query Match 86.0%; Score 1481.2; DB 15; Length 1991;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 138; Indels 5; Gaps 1;

QY 1 TGCACCAAGATGACTCTGAATGGACTTCAGTTCTTCTGTGTATACATCTCAGTTGTAC 60
DB 142 TGCACCAAGATGCTGTGAATGGACTTCAGTAATTTTGTCTAATCAACTGAGCTTTGC 201
QY 61 TTTAGCTCTGGAGTTCTGGAAGTGTCTGTGTGGCCGACAGAAACACACCATTTGGATG 120
DB 202 TTTAGCTCTGGGAATTTGTGGAAGGTGTCTGTGTGGGACAGAAACACACCATTTGGATG 261
QY 121 AATATGAAGACAAATCTCTGAAGAGCTTGTTCAGAGAGGTTCATGAGGTGACTGTACTGGCA 180
DB 262 AATATAAGACAAATCTCTGGATGAGCTTATTCAGAGGTTCATGAGGTGACTGTACTGGCA 321
QY 181 TCTTCAGCTTCCATTTCTTTTGTATCCCAATGATGATGCCATCTCTTAATTTGAAGTTTAT 240
DB 322 TCTTCAGCTTCCATTTCTTTTGTATCCCAACTCATCCGCTCTCTTAAATTTGAATTTAT 381
QY 241 CCTACATCTTTAACTAAACTGAATTTGAGAAATATCATCATGCAACAGGTTAAGAGATGG 300
DB 382 CCCACATCTTTAACTAAACTGTGTTGGAGAAATTTTCATCATGCAACAGATTAAGAGATGG 441

QY 301 TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTTCAAGAAACAAGAAATCCGTGG 360
DB 442 TCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTTCAAGATACAGGAATCATGTCA 501
QY 361 GAATTATATGACATATTTAGAAACTTCTGTGPAAGATGTAGTTTCAAAATAAGAAATGTTATG 420
DB 502 ATATTTGGTGACATAAATAGAAAAGTTCTGTGAAAAGATGTAGTTTCAAAATAAGAAATTTATG 561
QY 421 AAAAACTACAGAGTCAGANTTTGACATCGTTTTCAGATGCTGTGTTTCCCTGTGGT 480
DB 562 AAAAAAGTCAAGAGTCAAGATTGTGACGTCATTTTTCAGATGCTATTTTCCCTGTAGT 621
QY 481 GAGCTGCTGCTCGCTACTTAAACATACGGTTTGTGTACAGTCTTCCCTTTTACTCCCTGGC 540
DB 622 GAGCTGCTGCTGAGCTATTTAAACATACCTTGTGTACAGTCTCAGCTTCTCTCTGGC 681
QY 541 TACAAATTTGAAAGGACAGTGGAGGACTGATTTTCCCTCTCTTACATACATCTTATGTT 600
DB 682 TACACTTTTGAAGGACATAGTGGAGGATTTATTTTCCCTCTCTACGTACCTGTGTT 741
QY 601 ATGTCAAAATTAAGTATCAATGACCTTTTCATGGAGGGTAAATAATATGATCTATGTG 660
DB 742 ATGTCAAAATTAAGTATCAATGACCTTTTCATGGAGGGTAAATAATATGATCTATGTG 801
QY 661 CTTTATTTTACCTTTTGGTTTCCAAATGTCTGTATGAAGAGTGGGATCAGTTTATACAGT 720
DB 802 CTTTACTTTGACCTTTTGGTTTGAATATTTGACATGAAGAGTGGGATCAGTTTATAGT 861
QY 721 GAAGTTTGTAGGAAGACCCACTACTCTTATTTGAGCAATGGGAAAGCTGACATATGCTT 780
DB 862 GAAGTTCTAGGAAGACCCACTACTCTTATCTGAGCAATGGGAAAGCTGACATATGCTT 921
QY 781 ATGCGAACTCTCTGGAGTTTTCATTTTCTCATCTCTTACCAACGTTGATTTGTT 840
DB 922 ATTCGAACTCTCTGGAAATTTTTCAGTTTCTCTCATCTCTTACCAATGTTGATTTGTT 981
QY 841 GGAGGATTTCCACTGCAAAACCTGCAAAACCTTACCTAAGGAAATGGAGGAGTTTGTACAG 900
DB 982 GGAGGATCCACTGCAAAACCTGCAAAACCTTACCTAAGGAAATGGAGGAGTTTGTACAG 1041
QY 901 AGCTCTGGAGAAATGGTGTGTGTGTTTCTCTGGGTCAGTGTAAAGTAAACATGACA 960
DB 1042 AGCTCTGGAGAAATGGTGTGTGTTTCTCTGGGTCAGTGTAAAGTAAACATGACA 1101
QY 961 GCAGAAAGGCCAATCTAATGCAACAGCCCTTCCAAAGATCCCAAAAAGTTCTGTGG 1020
DB 1102 GAAGAAAGGCCAATCTAATGCAATCAGCCCTGGCCAGATCCCAAAAAGTTCTGTGG 1161
QY 1021 AGATTTGACGGGAATTAACACAGATGCTTAGGTCTCAATACTCGGCTGTACAAGTGGATA 1080
DB 1162 AGATTTGATGGGAATTAACACAGATACCTTAGGTCTCAATACTCGGCTGTATAGTGGATA 1221
QY 1081 CCCAGAAATGACCTTCTAGGTCTATCCAAAACACAGAGCTTTTATACTCATGTGGAGCC 1140
DB 1222 CCCAGAAATGACCTTCTAGGTCTATCCAAAACACAGAGCTTTTATACTCATGTGGAGCC 1281
QY 1141 AATGGCATCTATGAGGCAATCTACCATGGATCCCTATGTGGGCAATCCCATTTGTTT 1200
DB 1282 AATGGCATCTATGAGGCAATCTACCATGGATCCCTATGTGGGCAATCCCATTTGTTT 1341
QY 1201 GATCAACCTGATTAACATTTGCTCAATGAAGGCCAAGGAGCAGCTGTAGATTGGACTTC 1260
DB 1342 GATCAACCTGATTAACATTTGCTCAATGAAGGCCAAGGAGCAGCTGTAGATTGGACTTC 1401
QY 1261 AACCAATGTGAGTACAGACCTGTGAATGCACTGAAGCAGTAAATTAATGATCCCTTA 1320
DB 1402 AACCAATGTGAGTACAGACCTGTGAATGCACTGAAGCAGTAAATTAATGATCCCTTA 1461
QY 1321 TATAAGAGAAATATTAATAATTTATCAAGAAATTTCAACATGATCAACAGGTAAAGCCCTG 1380
DB 1462 TATAAGAGAAATATTAATAATTTATCAAGAAATTTCAACATGATCAACAGGTAAAGCCCTG 1521

Db 1343 TATAAGAGAAATGTTATGAATATCAAGAAATCAACATGATCAACGAGTGAAGCCCTG 1402
Qy 1381 GATCGAGCAGTCTTCGGATTGAATTTGTCATGCCCCACAAAGAGCCAAACACCTTCGA 1440
Db 1403 GATCGAGCAGTCTTCGGATTGAATTTGTCATGCCCCACAAAGAGTGAACACCTTCGG 1462
Qy 1441 GTTCGAGCCCATGACCTCAGCTGGTCCAGTACACACTCTTTGGATGATGATGGTTCTG 1500
Db 1463 GTTCGAGCCCATGACCTCAGCTGGTCCAGTACACACTCTTTGGATGATGATGGTTCTG 1522
Qy 1501 CTGCGCTGTGCGCACTGATATTTATCATCACAAAGTTTGTCTGCTTTGTTCTGCTGG 1560
Db 1523 CTGCTGTGTGGCACTGATATTTATCGTCACAAATGTTGTCTGTTTGTCTGCTGG 1582
Qy 1561 AAGTTTCTAGAAAAGGGAAGGGAAGAGATTAGTTATGCTCTGACATTTGAAGCT 1620
Db 1583 AAGTTTCTAGAAAAGGGAAGGGAAGAGATTAGTTATGCTCTGACATTTGAAGCT 1642
Qy 1621 GGAACCCAGATAGTAGGCAACTTCAGTTTATTCAGCAAGAAAGAAAGATTTGTTAT 1680
Db 1643 GGAACCCATGATAGGTGAGACTACTTCAGTTTATTCAGCAAG-----AAGATTTGTAT 1697
Qy 1681 GCAAGATTTCTTCTTC 1697
Db 1698 GCATGATGTCGATCTTC 1714

RESULT 14

US-10-450-763-5515
; Sequence 5515, Application US/10450763
; Publication No. US200501967541
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 5515
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (11)-(1597)
; OTHER INFORMATION: 98% homologous to Homo sapiens UDP-
; OTHER INFORMATION: glucuronosyltransferase, accession number X63359, Smith-Waterman
; OTHER INFORMATION: Score=2757.
US-10-450-763-5515

Query Match 84.4%; Score 1452.8; DB 24; Length 2802;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 1564; Conservative 0; Mismatches 142; Indels 6; Gaps 2;

Qy 1 TGCACACAGGATGACTCTGAATGACCTTCAGTTCTCTGCTGATACATCTCAGTTGTAC 60
Db 2 TGCACAGGATGGCTCTGAATGGACTACAG---TTCTGCTGATACACTCAGTTTAC 58
Qy 61 TTTAGCTCTGGAGTTGTGAAAAGTCTGGTGTGGCCCGCAGAAATACAGCCATTGGATG 120
Db 59 TTTAGCTCTGGAGTTGTGAAAAGTCTGGTGTGGCCCGCAGAAATACAGCCTTTGGATG 118
Qy 121 AATATGAAGACAATCCTGAAGAGCTTGTTCAGAGAGGTATGAGTGTACTGGCA 180
Db 119 AATATGAAGACAATCCTGAAGAGAACTTTGTTTACAGAGGTCATGAGGTGACTGTACTGGCA 178

Qy 181 TCTTCAGCTTCCATCTCTTTTGATCCCAATGATGATCCACTCTTAATAATTGAAGTTTAT 240
Db 179 TCTTCAGCTTCCATCTCTTTTGATCCCAAGACTCATCCACTCTTAACCTTGAAGTTTAT 238
Qy 241 CCTACATCTTTAACTAAACTGAATTTGAGATATCATCATGCAACAGGTTTAAGAGATGG 300
Db 239 CCTACATCTTTAACTAAACTGAATTTGAGATATCATCATGCAATTTGGTTAAAGATTC 298
Qy 301 TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAAGAACAAAGAAATCCCTGG 360
Db 299 TCAGAAATTCAAAAGATACATTTTGGTTACCTTTTTCACAAAGAACAAAGAAATCCCTGG 358
Qy 361 GAATATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAAGAAATGATG 420
Db 359 GCAATTAATGACATAATTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAAGAAATGATG 418
Qy 421 AAAAACTACAGAGTCAAGATTTGACATCGTTTTTTCAGATGCTGTTTTTCCCTGTGGT 480
Db 419 AAAAACTACAGAGTCAAGATTTGACATCGTTTTTTCAGATGCTGTTATTTACCCTGTGGT 478
Qy 481 GAGCTCTGGCTGGCTACTTAAACATACAGTTTGTGTACAGTCTCCGCTTTTACTCTCTGGC 540
Db 479 GAGCTCTGGCTGGCTACTTAAACATACAGTTTGTGTACAGTCTCCGCTTTTACTCTCTGGC 538
Qy 541 TACAAATTAAGAGGACAGTGGAGACTGATTTTCCCTCTCTTCTCATACTACCTTATGTT 600
Db 539 TACTCATTTTGAAGGCACAGTGGAGGATTTATTTCCCTCTCTTCTCAGTACCTGTTGTT 598
Qy 601 ATGTCAAAATTAAGTATCAATGACTTTTCATGGAGAGGTAAATAATATGATCTATGTC 660
Db 599 ATGTCAAAATTAAGTATCAATGACTTTTCATGGAGAGGTAAATAATATGATCTATGTC 658
Qy 661 CTTTATTTTGAATTTTGGTTTCCAAATGCTGTATGAAGAGTGGGATCAGTTTACAGT 720
Db 659 CTTTATTTTGAATTTTGGTTTCCAAATGCTGTATGAAGAGTGGGATCAGTTTACAGT 718
Qy 721 GAAGTTTGAAGAGACCCACTACTTTTATTTGAGACAAATGGGAAAGCTGACATATGCTT 780
Db 719 GAAGTTTGAAGAGACCCACTACTTTATCTGACAAATGAGGAAAGCTGACATATGCTT 778
Qy 781 ATGCGAAACTCTGGAGTTTCAATTTCTCTCATCTCTTCTTACCAAACGTTGATTTGTT 840
Db 779 ATGCGAAACTCTGGAGTTTCAATTTCTCTCATCTCTTCTTACCAAATGTTGATTTGTT 838
Qy 841 GGAGGATTCACCTGCAAACTCTGCAAACTCTTAAAGAAATGGAGAGTTTGTACAG 900
Db 839 GGAGGATTCACCTGCAAACTCTGCAAACTCTTAAAGAAATGGAGAGTTTGTACAG 898
Qy 901 AGCTCTGGAGAAATGGTGTGTGTGTTTCTCTGGGTCAGTGAATGAATGAATGAATGAAT 960
Db 899 AGCTCTGGAGAAATGGTGTGTGTGTTTCTCTGGGTCAGTGAATGAATGAATGAATGAAT 958
Qy 961 GCGAAAGGCCAATGATTAATGCAACAGCCCTTCCCAAGATCCCAAGAGTTCTGTG- 1019
Db 959 GAAGAAAGGCCAATGATTAATGCAACAGCCCTTCCCAAGATCCCAAGAGTTCTGTG 1018
Qy 1020 --GAGATTTGACGGGAATAAAACAGATGCTTAAAGTCTCAATCTCGGCTGTCAAGTGG 1077
Db 1019 GAGATTTGATGGGATTAACCAAGATGCTTAAAGTCTCAATCTCAATCTCAATCTCAATCT 1078
Qy 1078 ATACCCAGAGATGACCTTCTAGGTCTATCCAAACACAGAGCTTTTAACTCATGTGGA 1137
Db 1079 ATACCCAGAGATGACCTTCTAGGTCTATCCAAACACAGAGCTTTTAACTCATGTGGA 1138
Qy 1138 GCAATGGCATCTATGAGCAATCTACCATGGAATCCCTATGTTGGGCAATTCATTTGTT 1197
Db 1139 GCAATGGCATCTATGAGCAATCTACCATGGAATCCCTATGTTGGGCAATTCATTTGTT 1198
Qy 1198 TTTGATCAACCTGATTAACATTTGCTCAATGAAGCCAAAGGAGCAGCTGTAGATGGAC 1257
Db 1199 TTTGATCAACCTGATTAATTTGCTCAATGAAGCCAAAGGAGCAGCTGTAGATGGAC 1258
Qy 1258 TTCAACACAATGTGCGAGTACAGACCTGCTGAATGTCACCTGAAGAGCAGTAATTAATGATCTCT 1317

Db	1206	TGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGAGCAGCTGTTAGAGTGA	1265
Qy	1257	CTTCAACACAATCTCGAGTACAGACCTGCTGAATGCACCTGAAGACAGTAATTAATGATCC	1316
Db	1266	CTTCAACACAATCTCGAGTACAGACCTGCTGAATGCATGAAGAGAGTAATTAATGATCC	1325
Qy	1317	TTTATATAAGAGAATATTATGAAATTTATCAAGAAATTCACATGATCAACACAGTAAAGCC	1376
Db	1326	TTTCATATAAGAGAATGTTATGAAATTTATCAAGAAATTCACATGATCAACACAGTGAAGCC	1385
Qy	1377	CCTGGATCGAGCAGTCTTCTGGATTGAAATTTGTCATGCCCCACAAAGGAGCCAAACACCT	1436
Db	1386	CCTGGATCGAGCAGTCTTCTGGATTGAAATTTGTCATGCCCCACAAAGGAGCTAAACACCT	1445
Qy	1437	TCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCCTCTTTGGATGCTGATGGGTT	1496
Db	1446	TCGGGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCCTCTTTGGATGCTGATGGGTT	1505
Qy	1497	TCTGCTGGCTGTGTGGCAACTGTGATATTTATCATCAAAAGTTTGTCTGTTTTGTTT	1556
Db	1506	CCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAATGTTGTCTGTTTTGTTT	1565
Qy	1557	CTGGAAGTTTGTAGAAAAGGGAAGAGGAAAAGAGATTAGTTATGCTGACATTGA	1616
Db	1566	CTGGAAGTTTGTAGAAAAGGGAAGGAAAAGAGATTAGTTATGCTGAGATTGA	1625
Qy	1617	AGCTGGAACACAGATAGATAGGACAACCTTCAGTTTATTCAGCAAGAAAGAAAGATTG	1676
Db	1626	AGCTGGAACACCTGATAGGTGAGACTACTTCAGTTTATTCAGCAAG-----AAAGATTG	1680
Qy	1677	TTATGCAAGATTCTTTCTTCTGTCGACAAAAAAGAAAAA	1722
Db	1681	TGATGCAAGATTCTTTCTTCTGTCGACAAAAAAGAAAAA	1726

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Job time : 6782 secs

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